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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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binding antibody fragment (I), that preferentially binds cell-associated

CX 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also

CX 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also

CX a monoclonal antibody that competes with binding of (II); (3) a hybridoma

SX deposited in (II); (4) an isolated nucleic acid molecule (III)

CX as deposited in (II); (4) an isolated nucleic acid molecule (III)

CX antigen-binding antibody tragment that preferentially binds cell-

CX antigen-binding antibody fragment that preferentially binds cell-

CX antigen-binding antibody fragment that preferentially binds cell-

CX antigen-binding antibody or an antigen-binding monoclonal antibody fragment

CX (I); (5) a pharmaceutics (A 125/072P

CX (I); (5) a pharmaceutical composition comprising a

CX antigen-binding antibody or an antigen-binding monoclonal antibody fragment

CX (I); (5) a pharmaceutically binds cell-associated CA 125/0772P

CX (I); (6) a pharmaceutically binds cell-associated CA 125/0772P

CX (I); (7) an antibody, or an antigen-binding antibody fragment that

CX (I); (8) and a carrier contained within the packaging material, and

CX (I); (9) and pharmaceutically binds cell-associated CA

CX (I); (10) an antibody (VX) comprising an antibody, or an antigen-binding

CX (I); (10) a monoclonal antibody (VX) (Chosen from 325.1, 621.1, 633.1, 654.1, 725.1, 8G9, 77F10, 8A1, 8A63, 18C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9, 17H1, 4E7, 117.1, 36B.1, 446.1, 501.1, and 776.1 or its antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated antibody, or antigen-binding antibody fragment binding with cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.
Amino aci
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                                                                                                                                                                                                                                                           antibody; antigen-binding antibody fragment; cell-associated CA 125/0772P; monoclonal antibody; cytostatic; immunostimulant; mediator of largis; tunnor; cell proliferative disorder; cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
 Abp31025 Ada08747 Adf09090 B
                                                                                                                                                                                                                                125/0772P 3-repeat amino acid sequence SEQ ID NO:1.
                                                                         ALIGNMENTS
 ABP31025
ADA08747
ADF09090
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antibody fragment; (11) an antibody or antigen binding antibody fragment that competes with (VI); and (12) a pharmaceutical composition comprising (VI) and a carrier. (I) has cytostatic activity, and can be used as an immunostimiant and a mediator of lysis of positive tumour cell. (I) is useful for ameliorating a symptom of a CA 125/O77P-related disorder which is a cell proliferative disorder such as cancer, cervical or uterine cancer, breast or lung cancer or ovarian cancer. (V) is useful diagnostically for monitoring the development or progression of cancer or tumour as part of clinical testing procedure. The present sequence represents the CA 125/O772P 3-repeat amino acid sequence, which is used in the exemplification of the present invention.
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Best Local Similarity 100.
Matches 748; Conservative
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antibody; antigen-binding antibody fragment; cell-associated CA 125/O772P; monoclonal antibody; cytostatic; immunostimulant; mediator of lysis; tumour; cell proliferative disorder; cancer; cervical cancer; uterine cancer; breast cancer; lung cancer; ovarian cancer.
                                    CA 125/0772P 3-repeat TM amino acid sequence SEQ ID NO:2.
ADS94303 standard; protein; 809 AA
                                                                                                                                         16-OCT-2002; 2002US-0418828P
10-JUL-2003; 2003US-0485986P
                                                                                                                             15-OCT-2003; 2003WO-US032945
                         (first entry
                                                                                                                                                            (EURO-) EUROCELTIQUE SA.
                                                                                                                                                                        Albone EF, Soltis DA;
                                                                                                                                                                                     WPI; 2004-357171/33.
                                                                                                   WO2004035537-A2
                        02-DEC-2004
                                                                                                                29-APR-2004
                                                                                       Synthetic
            ADS94303
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Novel isolated antibody, or antigen-binding antibody fragment binding with cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.

Example; SEQ ID NO 2; 153pp; English

The present invention describes an isolated antiloody, or an antigen-binding antiloddy fragment (1), that preferentially binds cell-associated described: (1) a monoclonal antiloddy (II) produced by hybriddom 4E7; (2) a monoclonal antibody that competes with binding of (III); (3) a hybriddom 4E7; (2) a monoclonal antibody that competes with binding of (III); (3) a hybriddom 5C a deposited in (II); (4) an isolated mucleic acid molecule (III) comprising a nucleotide sequence that encodes a variable chain region of (I); (5) a pharmaceutical composition comprising an antibody fragment that preferentially binds cell-associated CA 125/0772P polypeptide relative to shed CA 125/0772P polypeptide relative to shed CA 125/0772P polypeptide cannoclonal antibody fragment that preferentially binds cell-associated CA 125/0772P polypeptide comprising an antibody or an antigen-binding antibody fragment that chart preferentially binds cell-associated CA 125/0772P polypeptide comprising an antibody or an antigen-binding antibody fragment that composition in a form suitable for administration to a subject; (8) a composition in a form suitable for administration to a subject; (8) a composition in a form suitable for administration to a subject; (8) a composition in a form suitable for administration to a subject; (9) antibody fragment, which preferentially binds cell-associated CA 125/0772P polypeptide (V) comprising an antibody or an antigen-binding antibody fragment, which preferentially binds cell-associated CA 125/0772P polypeptide (V) comprising or antibody or an antigen-binding cantibody fragment, which preferentially binds cell-associated CA 125/0772P relative to shed CA 125/0772P polypeptide (V) comprising or antibody fragment, which preferentially binds cell-associated CA 125/0772P related to shed CA 125/0772P related to shed CA 125/0772P related to shed CA 125/0772P related day antibody or antibody fragment, (II) and carrier (II) a monoclonal antibody or antipod carrier (II) and carrier (II) and carrier (II) and carrier (I present invention describes an isolated antibody, or

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61 ITMLRYBENNWPGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGV 120
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used in the exemplification of the present invention.
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92.5%;
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                                                       Query Match
Best Local Similarity 92.5'
                                 Sequence 809 AA;
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This invention relates to polypeptides comprising an immunogenic portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer.
                                                                                                                            438 PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWBLSQLTH
                                   GVIQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLIRDIQ
                                                    498 GVTQLGFYVLDRDSLFINGYAPQNLSIRGBYQINFHIVNWNLSNPDPTSSEYITLLRDIQ
                                                                                                         DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
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Hill P, Albone E;
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Carter D,
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2000US-00667857.
2001US-00827271.
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Vedvick TS,
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20-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention
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                                       Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
tumour antigen; identification; cytostatic; gene therapy; vaccine.
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   ovarian carcinoma antigen 0772P protein SEQ ID NO:389
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Pred. No. 2.2e-315;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                       Frudakis TN;
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                                                                                                                                                                                                                                                                                                                                                                         Algate PA,
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98US-00216003.
99US-00338933.
99US-00404879.
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Best Local Similarity 99.9%;
Matches 696; Conservative
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17-DEC-1998;
23-JUN-1999;
                                                                                                 Homo sapiens
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Fling SP, Hill P, Al

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The invention relates to an isolated 0772P polypeptide, which has the structure fully defined in the specification. The composition containing the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells or antigen presenting calls are useful for stimulating an immune response and treating ovarian cancer. Detecting the presence of the polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian carcinoma cDNAs and protein cDNAs were identified using microarray technology. The present sequence represents a human ovarian carcinoma
                                                                                                                                                                                                        New isolated 0772P polypeptides and polynucleotides, useful in gene therapy, particularly for treating or diagnosing cancer, e.g. ovarian cancer.
                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 389; 371pp; English
      18-JUN-2001; 2001US-00884441.
                                                                                                                                                     Mitcham JL, King GB,
Reed SG, Vedvick TS,
                        MITCHAM J L.
KING G E.
ALGATE P A.
FLING S P.
RETTER M W.
FANGER G R.
                                                                                                                                                                                    WPI; 2003-532352/50.
                                                                                      REED S G.
VEDVICK T &
CARTER D.
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  Score 3663; DB 5;
Pred. No. 2.2e-315;
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0; Mismatches 1;
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ilarity 99.9%;
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human; gene therapy; ovarian cancer; cancer Human ovarian carcinoma antigen 0772P

17-JUL-2001; 2001US-00907969

US2003091580-A1

15-MAY-2003

Homo sapiens

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samples, and therefore which patients may be in need of restorative therapy. The host cell may also be used as antigens in the production of antibodies against (II) and in assays to identify modulators of (II)'s expression and activity. The anti-(II) antibodies, agonists and antiagonists may be used to regulate expression and activity and as diagnostic agents for detecting the presence of (II) in samples (e.g. bimmunoassay). This sequence represents a secreted ovarian carcinoma
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                                                                                                                                                                                                                           FTHRSSUSTISTECTPTVYLGASKTPASI FGPSAASHLLILFTLNFTI TNLRYEENMWPG
                                                                                                                                                                     Score 3663; DB 7; : Pred. No. 2.2e-315; ); Mismatches 1;
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                                                                                                         677
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                                                                                                                                                                   737
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                    553
                                                                                                                                      NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                                                                                                       DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVBQVFLDKTLNASFH
                                                                          WLGSTYQLVDIHVTEMESSYYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; protein therapy; vaccine; antibody inhibition; breast cancer; restorative therapy; diagnostic agent; immunoassay; secreted ovarian carcinoma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids useful for the prevention, diagnosis and of breast cancer.
                                                                                                                                                                                                    LRMTRNGTOLONFTLDRSSVLVDGYSPNRNEPLTGNS
                                                                                                                                                                                                                   Secreted ovarian carcinoma antigen seqid 389
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980S-00216003.
990S-0039933.
2000S-00404879.
2000US-0061747.
2000US-00658801.
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2001US-00884441.
2001US-00907969.
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N-PSDB; ADF08882.
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10-AUG-2000; 2
20-SEP-2000; 2
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23-JUN-1999;
24-SEP-1999;
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433 497

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557 553

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The invention relates to an isolated polynucleotide comprising a sequence of, a sequence hybridizing under highly stringent conditions to, or having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
                                                                                                                                                                                                                                                                                                                                  618 WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLFYSQDKAQPGTTNYQRNKR 677
                 PLPQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433
                                      GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing, preventing and treating diseases, such as ovarian cancer, and for eliciting humoral and/or cellular immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian carcinoma antigen cDNA 0772P clone 21003 encoded protein.
                                                                                                                      498 GVTQLGFYVLDRDSLFINGYAPQNLSIRGRYQINFHIVNWNLSNPDPTSSEYITLLRDIQ
                                                                                                                                                                                 DKVTTLYKGSQLHDTPRPCLVTNLTMDSVLVTVKALPSSNLDPSLVBQVFLDKTLNASFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis, cytostatic, immunostimulant, gene therapy; tumor, ovarian tumor, cancer, carcinoma, antigen.
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17-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                              요
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Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
cytostatic; 0772P.
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Pred. No. 2.2e-315;
0; Mismatches 1;
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23-UTN-1999; 990S-00338933.
24-SER-1999; 990S-00404879.
17-UTL-2000; 2000US-0061747.
10-AUG-2000; 2000US-0063891.
20-SEP-2000; 2000US-0065881.
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Best Local Similarity 99.9%;
Matches 696; Conservative
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(FANG/) FANGER
                                                                  Homo sapiens
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                                                                                                                                             FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENNWPG 137
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the specification, its complement or degenerate variants, or a sequence of at least 20 contiguous residues of the 849 or 1399 bp sequence. The polynucleotides and polypeptides are useful for diagnosing, preventing and treating diseases, such as ovarian cancer, and for eliciting humoral and/or cellular immune response. This sequence corresponds to an ovarian carcinoma antigen protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                                                                                                                                                        GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGPTHRSSVPTTSTGVVSEEPPTLNFT
                                                                                                                                                                                                                                               INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGABTR
                                                                                                                                                                                                                                                           VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                                                                                                                                   TPKPATTFLPPLSBATTAMGYHLKTLTLNFT1SNLQYSPDMGKGSATFNSTEGVLQHLLR
                                                                                                                                                                                                                                                                                                                                         PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
                                                                                                                                                                  74 SRKFNTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP
                                                                                                                                                                                                                   FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG
                                                                                                          Gaps
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                                                                                                          IndelB
                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710
                                                                                      Score 3663; DB 9;
Pred. No. 2.2e-315;
0; Mismatches 1;
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99.9%;
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                                                                       Sequence 833 AA;
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434 GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polypucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human everain carcinoma polymucleotides and proteins used in the exemplification of the present invention
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Pred. No. 2.5e-315;
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                                                                                                                                                                                                                                                                                               cancer, preferably ovarian cancer
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                                                                                                                      98US-00215681.
98US-00216003.
99US-00338933.
99US-00404879.
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Matches 696; Conserv
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                                                WO200036107-A2
                          Homo sapiens,
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17-DEC-1998;
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ovarian carcinoma; ovarian cancer; therapy; diagnosis;

Human;

Human ovarian carcinoma antigen 0772P protein SEQ ID NO:312.

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                                   279 GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT
                                                                                             SRKFNTTERVLOGILRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP
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             FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWWPG
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10-AUG-2000; 2000US-00636801.
20-SEP-2000; 2000US-00667857.
04-APR-2001; 2001US-00827271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; human; breast tumour protein; breast cancer; ovarian tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       them, useful
DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                                  WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                     WLGSTYQLVDIHVTEMBSSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                                                                      NI EDALINQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                                                                                                                                                                                                               NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPLARRVDRVAIYEEF
                                                                DKVTTLYKGSQLHDTPRPCLVTNLTMDSVLVTVKALPSSNLDPSLVEQVPLDKTLNASFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast tumor polypeptides and the nucleic acids that encode t for the prevention, diagnosis and treatment of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 914;
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Pred. No. 2.5e-315;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ovarian tumour-derived antigen 0772P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 914
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22-FEB-2000; 2000US-00510662.
10-MAR-2000; 2000US-0053586.
07-APR-2000; 2000US-00545068.
15-MAY-2000; 2000US-00571025.
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Best Local Similarity 99.9
Matches 696; Conservative
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194 INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR 253
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18-JUN-2001;
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20-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVTQLGFYVLDRDSLFINGYAPQNLSIRGEXQINFHIVNWNLSNPDPTSSEXITLLRDIQ
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                                                                                                                 Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in patient and treating ovarian cancer.
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                                             Fling SP, Retter MW,
Hill P, Albone E;
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Pred. No. 2.5e-315;
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                              PA,
D,
                                               Algate
Carter
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18-JUN-2001; 2001US-0088441
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nes 696; Conservative
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                        (CORI-) CORIXA CORP
                                                                                 WPI; 2002-164781/21.
N-PSDB; ABN72974.
                                              JL, King (
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Reed SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in spatient and treating ovarian cancer.
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Hill P, Albone E;
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Pred. No. 2.5e-315;
0; Mismatches 1;
                              819 LEMTRNGTQLQNFTLDRSSVLVDGYFPNRNEPLTGNS
LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS
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Carter D, <sup>1</sup>
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2000US-00667857.
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2001US-00884441.
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Reed SG, Vedvick TS,
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                                                                                                                                        PLPOKSSMGPPYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433
                                                                                                                                                                                         GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
                                                                                                                                                                                                              GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 638
                                                                                                                                                                                                                                        DKVTTLYKGSQLHDTPRPCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVPLDKTLNASFH 553
                                                                                                                                                                                                                                                                 DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 698
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                                                    399 VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                      459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
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                                       VDLLCTYLQPLSGPGLP1KQVFHELSQQTHG1TRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; gene therapy; vaccine; breast cancer; cancer; tumour; immune response; 08E; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                         LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breast cancer associated polypeptide segid 206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADU01425 standard; protein; 914
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22-FEB-2000; 2000US-00510662.
10-MAR-2000; 2000US-0052386.
07-APR-2000; 2000US-00545608.
15-MAY-2000; 2000US-00541025.
06-FEB-2001; 2001US-00779320.
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MITCHAM J L.
WANG T.
MCNEILL P D.
HARLOCKER S L.
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JIANG Y.
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The invention describes an isolated breast cancer polymucleotide (I) comprising a sequence (SI) selected from the 249 mucleotide sequence (II) defined in the specification, complements of SI, a sequence that fully defined in the specification, complements of SI, a sequence that the specification comprising at least 20 contiguous residues of SI, a sequence that the comprising at least 75%, preferably 90% identity to SI, or degenerate variants of SI. Also described are: an isolated polypeptide (II) encoded by (I), or expression vector (III); a host cell (V) transformed or transfected with certain isolated antibody (Ab) that specifically binds to (II); an isolated antibody (Ab) that specifically binds to (II); detecting (MI); an oligonucleotide (VI) that hybridiess to SI; detecting (MI); an oligonucleotide (VI) that hybridiess to SI; detecting (MI); an oligonucleotide (VI) that hybridiess to SI; detecting (MI); an oligonucleotide (VI) that hybridiess to SI; detecting (MI); an antispop presenting cells that express (II); a composition (C) comprising physiologically acceptable carriers and inhibiting (M3) the development of a cancer in a patient. (V) is an antispop presenting cells that express (II); and inhibiting (M3) the development of a cancer in a patient. (VI) is an eaful for determining the presence of cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with a monoclonal antibody that binds to OSE, isolating cells that bind to the antibody that binds to OSE, isolating polymucleotides from the isolated cells, and comparing the amount of polymucleotides with (VI), detecting an encount polymucleotides with (VI), detecting an encount polymucleotides with (VI) are useful in pharmaceutical compositions. (C) is useful for cut-off value, and thus determining the presence of cancer in a patient, and thus determining the presence of cancer in a patient. (I) is useful for detecting the presence of cancer in a patient. (I) is useful for detecting the presence of cancer
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                                                                                                                                   Novel breast cancer polynucleotides and polypeptides encoded by the polynucleotides, useful for detecting the presence of breast cancer in patient, and in pharmaceutical compositions, for treating breast cancer.
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    Mitcham JL, Wang T;
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Pred. No. 2.5e-315;
0; Mismatches 1;
Day CH, Jiang Y, Houghton RL,
Harlocker SL;
                                                                                                                                                                                                                          Claim 2; SEQ ID NO 206; 159pp; English.
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il Similarity 99.9%;
696; Conservative
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  Dillon DC,
Mcneill PD,
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Matches 696
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VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT 458
                                                                                                                            GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
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                                                                                         PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGFGLDIQQLYWELSQLTH
                                                                                                                                             GVTQLGFYVLDRDSLFINGXAPQNLSIRGEYQINFHIVWWLSNPDPTSSEYITLLRDIQ
                                                                                                                                                                                                DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                                                                                                                                                                               TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
                                        TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
                                                                                                                                                                              DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                                                                                                                WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                                                                                        WLGSTYQLVDIHVTEMESSVYQPTSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                          PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; vaccine; diagnosis; pharmaceutical; cancer; neoplasm; breast tumor; endocrine disease; gynecology and obstetrics.
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Fanger GR;
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Zehentner B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human breast cancer associated protein SEQ ID NO 206.
                                                                                                                                                                                                                                                                                                                                    LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS 710
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Bennington AA,
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20-JUL-2001; 2001US-00910689.
30-NOV-2001; 2001US-00010742.
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Harlocker SL,
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Mcneill PD,
Retter MW;
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The invention describes an isolated breast cancer polynucleotide (I) comprising a sequence (SI) selected from the 249 nucleotide sequences

Claim 2; SEQ ID NO 206; 237pp; English.

comprising at least 20 contiguous residues of S1, a sequence that hybridize to S1, under moderately stringent conditions, a sequence that hybridize to S1, under moderately stringent conditions, a sequence that hybridize to S1, under moderately stringent conditions, a sequence having at least 75%, preferably 90% identity to S1, or degenerate variants of sequence (S2) selected from any one of the 11 sequences mentioned in the specification, sequences encoded by (1), or sequences having at least (CC 70%, preferably 90% identity to (1); an expression control sequence; a host comprising (1), operably linked to an expression control sequence; a host comprising (II), perably linked to an expression control sequence; a cell (IV) transformed or transfected with (III); an isolated antibody (A) of the interpretably linked to an expression control sequence; an isolated T cell population (VII), comprising (II); an oligonuclectide (VI) that specific for a tumor protein; an isolated T cell population (VII), comprising T cells prepared by (M2); an isolated T cell population (VII), comprising T cells prepared by (M2); an isolated T cell population (VII), comprising T cells prepared by (M2); an isolated T cell population (VII), comprising T cells prepared by (M2); an isolated T cell population (VII), comprising T cells prepared by (M2); and industring the development of a diagnostic kit (VIII) comprising (VI), or Ab and a detection reagent comprising a reporter group; and inhibiting (M3) the development of a patient, and therefore inhibiting presenting cells that express (II), so that T cell proliferate, administering the proliferated T cells to the compositions comprising are disclosed; monitoring the progression of dagnostic methods. (C) is useful for stimulating immune response in a patient, and for treating antisense oligonuclectide; and kit for use in dagnostic methods. (C) is useful for stimulating in patient of in pharmaceutical compositions.

CC determining the presence of cancer in a patient of a cancer in the cumor pol cancer. (C) is useful for inhibiting the development of breast cancer in a patient, and for removing tumor cells from a biological sample. Ab (binding agent for (I)) is useful for detecting the presence of cancer in a patient. This is the amino acid sequence of a breast cancer associated protein. Note: This sequence has been extracted from the sequence listing of a corrected version of the specification published on the 3rd of March 518 218 133 278 193 253 313 458 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373 374 PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433 398 73 INNLRYMADMGQPGSLKFNITDNVMGHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT SRKFNTTERVLQGLLRPLFKNTSVGPLYSGGRLTLLRPEKDGEATGVDAICTHRPDPTGP VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT PTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMMPG SRKFWITTERVLOGLIARPLFKWTSVGPLYSGCRLTLIARPEKDGEATGVDAICTHRPDPTGP Gaps ; 0 92.9%; Score 3663; DB 5; Length 914; 99.9%; Pred. No. 2.5e-315; ive 0; Mismatches 1; Indels 0 Conservative Similarity Sequence 914 AA; Best Local Simi 14 159 74 219 134 279 194 339 254 399 314 459 Query Match 셤 ò a ò 용 ò 용 ò 원 à ò 셤 8

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699 WLGSTYQLVDIHVTEMESSYYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 758
  and treating ovarian cancer. Detecting the presence of the polymorlectides and polymorles is useful for diagnosing cancer. Ovar carcinoma cDNAs and protein cDNAs were identified using microarray technology. The present sequence represents a human ovarian carcinoma.
                                                                                                                                                                                                                                                                                      159 FIHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYERNWWPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSERPFTLNFT
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                                                                                                                                                                                                                                                             14 PTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYBENMWPG
                                                                                                                                                                                                                                                                                                                                                   SRKFNTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGBATGVDAICTHRPDPTGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 TPKPATTFLPPLSBATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTBGVLQHLLR
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                                                                                                                                                                      Score 3663; DB 7;
Pred. No. 2.5e-315;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian carcinoma antigen 0772P
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                                                                                                                                                                        ch
il Similarity 99.9%;
696; Conservative
                                                                                                                                  Sequence 914 AA;
                                                                                                                                                                        Query Match
Best Local S:
Matches 696
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WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTTNYQRNKR
                                                                                            GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDFTSSEYITLLRDIQ
                                                                                                                                                      DKVTTLYKGSOLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                                                               DKVTTLYKGSQLHDTFRPCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                                                                                                                                                                                                                                     NIEDALMOLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                   GVTQLGFYVLDRDSLFINGYAPQNLSIRGRYQINFHIVNWNLSNPDPTSSEYITLLRDIQ
                                                                                                                                                                                                                                         WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                                                                                                                                                            NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated 0772P polypeptides and polymucleotides, useful in gene therapy, particularly for treating or diagnosing cancer, e.g. ovarian
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Hill P, Albone E;
                                                                                                                                                                                                                                                                                                                                                                                                                  LRMTRNGTOLONFTLDRSSVLVDGYSPNRNBPLTGNS 710
                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; gene therapy; ovarian cancer;
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Carter
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RETTER M W.
FANGER G R.
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ALGATE P A.
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VEDVICK I S
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Vedvick '
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HILL P.
ALBONE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003091580-A1
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(KING/)
(ALGA/)
(FLIN/)
(RETT/)
(FANG/)
(REED/)
(VEDV/)
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(ALBO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
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ADA08631
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                                                                                                                             DXVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLAASFH
                                                                                                                                              PLFOKSSMGPFYLGCQLISLRPEXDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
                           519 PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDFVGPGLDIQQLYWELSQLTH
                                                                  GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ
                                                                                     554 WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                                                                                                                                                                      NIEDALWQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                                                                                                                                                                                                                          gene therapy; protein therapy; vaccine; antibody inhibition; breast cancer; restorative therapy; diagnostic agent; immunoassay; secreted ovarian carcinoma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogenic nucleic acids useful for the prevention, diagnosis and treatment of breast cancer.
                                                                                                                                                                                                                                                                                                                    710
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                                                                                                                                                                                                                                                                                                                    LEMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS
                                                                                                                                                                                                                                                                                                                                    Secreted ovarian carcinoma antigen seqid 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF08974 standard; protein; 914
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98US-00216003.
99US-0038933.
90US-0048793.
2000US-00617747.
2000US-00636801.
2000US-00636801.
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2001US-00907969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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18-JUN-2001;
17-JUL-2001;
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17-DEC-1998;
23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGRATGVDALCTHRPDPTGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRKFNTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.9%; Score 3663; DB 7; Length 9 .larity 99.9%; Pred. No. 2.5e-315; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                         Fling SP, Retter MW,
Hill P, Albone E;
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                                                                                                                                                                                                                                                                                                                                         Algate PA,
Carter D,
                                                                                        17-JUL-2001; 2001US-00907969
                                                                                                                     18-JUN-2001; 2001US-0088441
                                                                                                                                                               KING G E.
ALGATE P A.
FLING S P.
RETTER M W.
FANGER G R.
REED S G.
                                                                                                                                                                                                                                                                                                                                         Mitcham JL, King GE,
Reed SG, Vedvick TS,
                                                                                                                                                    MITCHAM J L.
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N-PSDB; ADA09060.
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696; Conserv
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HILL P.
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(RETT/)
(FANG/)
(REED/)
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(CART/)
(HILL/)
(ALBO/)
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Matches
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standard; protein; 914

(first entry)

12-FEB-2004

ADF08808; ADF08808

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cancers. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient segment that affect the activity of (II) by expressing inactive proteins or to supplement the patients own production of (II).

Additionally, (I) may be used to produce (II), by inserting (I) into a complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative therapy. The host cell may also be used as antigens in the production of antibodies against (II) and in assays to identify modulators of (II)'s expression and activity. The anti-(II) antibodies, agonists and chargonists may be used to respression and activity and as chargonists may be used to regulate expression and activity and as diagnostic agents for detecting the presence of (II) in samples (e.g. by imminoassay). This sequence represents a secreted ovarian carcinoma
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## Sequence 914 AA;

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                                                                                                                                                                                                    GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
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                                                                                    FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLKYEENMMPG
                                                                                                                                                     SRKFWITERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP
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                                                                                                                                    SRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPBKDGEATGVDAICTHRPDFTGP
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92.9%; Score 3663; DB 7; Length 914; 99.9%; Pred. No. 2.5e-315; ive 0; Mismatches 1; Indels (
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                 Best Local Similarity 99.9
Matches 696; Conservative
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gene therapy, protein therapy, vaccine, antibody inhibition; breast cancer; restorative therapy, diagnostic agent, immunoassay; secreted ovarian carcinoma antigen.
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                                                                                                                                                                                               Secreted ovarian carcinoma antigen seqid 312.
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98US-00216003.
99US-00338933.
99US-00404879.
2000US-00617747.
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2001US-00827271.
2001US-00884441.
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N-PSDB; ADF08807.
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17-DEC-1998;
23-JUN-1999;
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ADF 08808

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YXX BR 17-1

YXX BR 17-1

YXX BR 17-1

YXX BR 117-1

YXX BR 117-1

YXX BR 24-1

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## Example 2; SEQ ID NO 312; 399pp; English.

The invention describes nucleic acids (I) and the polypeptides (II) they encode. The nucleic acids (I) may be used for preventing, diagnosing and treating diseases related to their aberrant expression i.e. breast cancers: For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (II) by expressing in circiive proteins or to supplement the patients own production of (II). Additionally, (I) may be used to produce (II), by inserting (I) into a host cell and culturing the cell to express the protein (II). (I) And its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative therapy. The host cell may also be used as antigens in the production of antibodies against (II) and in assays to identify modulators of (II)'s expression and activity. The anti-(II) antibodies, agonists and cativity and as antigonists may be used to regulate expression and activity and as diagnostic agents for detecting the presence of (II) in samples (e.g. by immunoassay). This sequence represents a secreted ovarian carcinoma

## Sequence 914 AA;

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 Length 914;
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Score 3663; DB 7;
Pred. No. 2.5e-315;
0; Mismatches 1;
  92.9%;
  Query Match
Best Local Similarity 99.9
Matches 696; Conservative
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DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
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Matches 696; Conservative
                                       Retter MW, Fanger GR;
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                                                               N-PSDB; ADG46555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ovarian carcinoma; OBE; ovarian cancer; secreted tumour antigen; cytostatic; 0772P.
                                                                                                                                                                                    SRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP
                                                 GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT
                                                                                 VDLLCTYLQPLSGPGLPIKQVFHELSQQTFGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                        INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
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98US-00316003.
99US-00438933.
99US-00404879.
2000US-0061747.
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17-JUL-2000;
10-AUG-2000;
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The invention relates to human ovarian carcinoma polypeptides, designated OBE or 0772P, and the polymucleotides encoding them. The invention also relates to methods for inhibiting the development of cancer, e.g. ovarian cancer in a patient, methods for stimulating and/or expanding T cells and methods for identifying secreted tumour antigens. The polypeptides, compositions, antibodies to the polypeptides and methods are useful for diagnosing, preventing, treating and monitoring cancer, e.g. ovarian cancer. The composition is particularly useful for stimulating an immune response in patient. This sequence represents a human ovarian carcinoma polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                      New isolated OBE or 0772P polypeptides, useful for diagnosing, preventing, treating and monitoring cancer, e.g. ovarian cancer, stimulating the immune response in patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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99.9%; Pred. No. 2.5e-315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; SEQ ID NO 312; 290pp; English
20-SEP-2000; 2000US-00667857
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193

253 398 313 458

278

133

73

373

518 433 578 493 638 553 758

Gape

Length 914; Indels

2.5e-315; DB 8;

92.9%; llarity 99.9%; Conservative

Query Match

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The present invention relates to polynuclectide and polypeptide sequences associated with breast cancer. Also disclosed are expression vectors comprising the polynuclectide sequences of the invention operably linked to an expression control sequence, host cells comprising the vector, antibodies (or antigen binding fragments of antibodies) specifically binding the polypeptides of the invention, fusion proteins comprising at least one of the polypeptides, stimulating and/or expanding T cells specific for a tumour protein. The polynuclectide sequences, polypeptide sequences, and antigen presenting cells can be administered they can be included with a physiological carrier/immunostimulant in compositions such as vaccines, particularly to treat or prevent cancers such as breast cancer. They can also be used to inhibit the development of cancer by incubating one or more of them with CD4+ and/or CD8+ T cells isolated from a patient, such that the T cells proliferate, and administering the producing one or more of them with CD4+ and/or CD8+ T cells isolated from a patient, such that the T cells proliferate, and administering the useful for detecting cancer in a patient, producing fusion proteins, producing T cell populations and antigen presenting cells. The present sequence represent
 673
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                                                                                                                                                                                                                                                                                                                                                           Human; breast cancer; T cell; tumour protein; antigen presenting cell;
immune response; CD4+; CD8+; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides, useful for treating and diagnosing cancer, particularly breast cancer by stimulating immune response in a patient and inhibiting the development of cancer.
NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                       759 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNPSPLARRVDRVAIYEEF
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22-FEB-2000; 2000US-00510662.
10-MAR-2000; 2000US-0052386.
07-APR-2000; 2000US-00545068.
15-MAY-2000; 2000US-00571025.
06-FEB-2001; 2001US-00778320.
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N-PSDB; ADN40450.
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

March 20, 2006, 07:28:38 ; Search time 140.158 Seconds (without alignments) 3765.293 Million cell updates/sec Run on:

US-10-687-035-1 3945 1 AAQPARRARRIKLFTHRSSV.....QKLISEEDLNMHTGHHHHHH 748 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

UniProt\_05.80:\*
1: uniprot\_sprot:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                         MEDLINE=21347965; PubMed=11369781; DOI=10.1074/jbc.M103554200; Xin B.W., Lloyd K.O.; White M.O.; Lloyd K.O.; "Molecular cloning of the cal25 ovarian cancer antigen. identification as a new mucin, mucin."; Biol. Chem. 276:27371-27375(2001).
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AFS61486; AAK74120.3; -; mENA.
HSSP; Q9D1H1; 11VZ.
                                                                                                       Last sequence update)
Last annotation update)
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larity 99.9%; Pred. No. 2.7e-237;
Conservative 1; Mismatches 0;
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PROSITE; PS50024; SEA; 6.
NON TER 1 1 SEQUENCE 6995 AA; 74495R MW. DATTONNOWN 1.
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Ensembl; ENSG00000181143; Homo sapient
InterPro; IPR000194; ATPase_a/bcentre.
InterPro; IPR000094; SEA.
Fram; PF01390; SEA; 20.
SMART; SM00200; SEA; 10.
                                          PRT;
                                                                                     Created)
                                                                                 01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
                                    Q96RK2_HUMAN PRELIMINARY;
Q96RK2;
                                                                                                                                                                                               Homo sapiens (Human)
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Name=MUC16;
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tes 696; Conserv
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5660 GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 6719
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                    554 WIGSTYOLVDIHVTEMESSVYOPTSSSSTOHFYLNFTITNLPYSODKAOPGTTNYORNKR
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"The CA 125 gene: an extracellular superstructure dominated by repeat
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MEDLINE=21646939; PubMed=11786729; DOI=10.1159/000050638;
O'Brien T.J., Beard J.B., Underwood L.J., Dennis R.A., Santin A.D.,
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PROSITE; PS00152; ATPAGE ALPHA_BETA; UNKNOWN_1.
PROSITE; PS50045; SEÅ; 11.
SEQUENCE 22152 AA; 2352668 MW; B3E7BDF19997A440 CRC64;
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF414442; AAL65133.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2004 (TrEMBLrel. 23, Last sequence update) Ovarian cancer related tumor marker CA125.
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Ensembl; ENSG00000181143; Homo sapiens.
HGNC; HAGNC:15582; MUC16.
InterPro; IPR000194; ATPase_a/bcentre.
InterPro; IPR000082; SEA.
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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Tumour Biol. 22:348-366(2001).
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Best Local Similarity 99.7
Matches 695; Conservative
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OBHIST;
OBHIST;
OBHIST;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ14303.
Hypothetical protein FLJ14303.
Hymon sapiens (Human)
Ewkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                            PLFOKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
                                                                                 21637 VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGLDEPPT
                                                                                                                                       TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDWGKGSATFNSTEGVLQHLLR
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                    INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
                                                                                                                                                                                                                                            GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ
INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
                                                            VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                  PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
                                                                                                                                                                                                                                                                                                            DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
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PubMed=14702039; DOI=10.1038/ng1285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
                         Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
Mizushiima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
"Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 SRKFNTTERVLQGLLRPLFKNTSVGPLYSGSRLTLLRPBKDGBATGVDAICTHRPDPTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          753 PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
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Fujiwara T.,
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M
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Pred. No. 6.4e-237;
0; Mismatches 3;
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   Fujimori Y., Komiyama M., Tashiro H.,
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Pram; PF01390; SEA; 7.
PROSITE; PS50024; SEA; 3.
SEQUENCE 1148 AA; 127957
                                                                                                                                                                                                                                                                                                                               Nat. Genet. 36:40-45(2004).
EMBL; AX024365; BAB14899.1;
HSSP; Q9D1H; 11VZ.
SMR; Q9HS77; 956-1075.
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Best Local Similarity 99.6
Matches 694; Conservative
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546 -KTLNASFHWLGS-TYQLVDIHVTEMESSVYQPTSSS---STQHFYLNFTITNLPYSQDK 600
                                    492 IQDKVTTLYKGSQLHDTFRFCLVTNL--TMDSVLVTVKALFSSNLDPSLV----EQVFLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                         Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
A Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
A Matsumura Y., Moriya S., Chiba E., Momyama H., Onogawa S.,
A Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Katsoka R.,
Kuga N., Kuroda A., Satoh I., Kamata K., Takami S., Terashima Y.,
A Matanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
Kikuchi H., Kanda K., Wagatsuma M., Murakawa R., Kanehori K.,
A Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

BRBL, AK126681, BAC875681; -, MRNA.
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                                                                                                                                            Hypothetical protein FLJ46845.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTHRNEVPITSTPGTSTVHLGTSETPSSLPRPIVPGPLLVPFTLNFTITNLQYEEAMRHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      867 AA; 96200 MW; C7B3033258839622 CRC64;
                                                                                                   Last sequence update)
Last annotation update)
                                      867 AA
                                         PRT;
                                                                                  Created)
                                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000082; SEA.
Pfam; PF01390; SEA; 4.
PROSITE; PS50024; SEA; 2.
                                      QGZQWS_HUMAN PRELIMINARY;
QGZQWS;
                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                   TISSUE=Uterus;
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Best Local Simi:
Matches 356; (
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NUCLEOTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUB=Whole body;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Komoo H., Adachi J., Fukuda S.,
Arakawa T., Cawa M., Nishi K., Kiyosawa H., Komoo S., Yamanaka I.,
Asaito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A, Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A, Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
Relischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Aschriml L.M., Staubli F., Suvuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Cantinic P., de Bonaldo M.P.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Nambar-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
699 LSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADM 758
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 19-day embryo whole body cDNA, RIKBN full-length enriched
11brary, clone:1110008114 product:hypothetical SEA domain containing
protein, full insert sequence.
                                                                                                                                                           601 AQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNF-SP
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Buarchontoglires, Glires; Rodentia; Sclurognathi,
Muroidea, Muridae, Murinae, Mus.
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
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Hanagaki T., Hara A., Hayatau N., Hiramoto K., Hiraka T., Kato H.,
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Mayazaki Y., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
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Muramatsu M., Hayashizaki Y.,
I. Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL, AKO03577; BAB22869.1; -; mRNA.
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                                        MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Muramatsu M., Hayashizaki Y.; Shibata M., Payashizaki Y.; Dibata Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                STRAIN=C57BL/63; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

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"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
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MGI; MGI:1920982; 1110008114Rk.
                              STRAIN=C57BL/6J; TISSUE=Whole body;
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SEQUENCE 258 AA; 29426 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 YQINFHI---VNWNLSNPDPTSSEYITLLRDIQDKVTTLYKGSQLHDTFRFCL-VTN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1408;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAN-2004 (TrEMBLrel. 26, Last annotation update)
01-MAN-2004 (TrEMBLrel. 26, Last annotation update)
Cell surface glycoprotein (S-layer protein) related protein.
OrderedLocusNames=MTH1513,
Methanobacterium theramoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LIMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFHWLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 NFTVT-----PDACKKNLTGLSDGFLTRFTPFIISNISVTPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1408 AA; 152736 MW; 294EC7742ABB29F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deltaH: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.7%; Score 144.5; DB 2;
20.1%; Pred. No. 1.9;
tive 99; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 179:7135-7155(1997).
EMBL; AE000911; AAB85988.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 SVPTTSTGVVSEEPFTLNFTI-----
                                                                                                                                                                                                                                                                                                                                             STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7155 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR010620; SBBP. Pfam; PF06739; SBBP; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 20.14
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; H69068; H69068.
                                                                                                                                                                                                                                           NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
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635

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PubMed=15155910; DOI=10.1073/pnas.0402414101;
PubMed=15155910; DOI=10.1073/pnas.0402414101;
PubMed=15155910; DOI=10.1073/pnas.0402414101;
PubMed=15155910; DOI=10.1073/pnas.040.C.U. Chapman G.D., Chute M.D.,
Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
Maitone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
Popovic T., Fraser C.M.;
"Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax.";
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).
C. -! CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

C. Preliminary data.
C. Ball: AakKoll000009; Ball5315.1; -; Genomic DNA.
SEQUENCE 5010 AA; 521891 MW; B00914651BF832DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |::|||::| | | 3819 | 3760 SSAMYQYVSIPTAPPVNRSATSNIVTTSLQNANIISIKQADVTFVSIGQNITYTNTLQNI 3819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : | : | : | : | : | SIPAGTTFVPDSVTINGVLQPDTNPENGISIGTIPSNSSKTILFQVQTNNPPTETBIVNQ 3759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MWPGSRKFNTTERVLQGLLRP---LFKNTSVGPLYSGCRLTLL-----RPEKDGEATG- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPYTLD-------RDSLYVNGFTHRSSVP---TTSTGVVSEEPFTLNFTINN 196
                                                                                                                                                                                                                                                                                                                447 MNATY---PDSHAARHDTLNKDGIIQYQTIVFTNFKSEADRIFRYFDDMRYRVAVIHGDM 503
                                                                                                                                                                                                            ------ 446
                                                                                                                                                                                                                                                                                                                                                                      675 RMTRNGTQLQNFTLDRSSVLVDGYSPNR------NEPLTGNSADIQHSGGRSSLE 723
                                                                                                                                                                                                                                                                                                                                                                                                                      504 TOKERENNLKYFKAGRINILIGTDVAQRGLDIPNVRLVLNYDLPGNVDDYTHRIGRTGRA 563
320 HELPPIHHSVQ-DPSNPDITHQ-----IERQTLLFSATFPKE-----IKNLAMEF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 RIKLFIHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYBEN
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                                                     ----SVLVTVKALFSSNLDPSLVEQVFLDKTLNASFHWLGSTYQLVDIHVTEMESSVYQ
                                                                                                                                                            576 PTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDC
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                                                                                                                                                                                                                                                                  -------CNFSPLARRV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 141.5; 18.5%; Pred. No. 21;
                                                                                                                                                                                                            -TEYITGONADLNNMLIEV-YGTDKEO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                     636 QVSTFRSVPNRHHTGVDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q4MT18_BACCE PRELIMINARY;
Q4MT18;
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ORFNames=BCE G9241 1620;
Bacillus cereus G9241.
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Matches 153; Conserv
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214 AKGSRAYPFC--IIMSPTRELVQQTAKASWML------SYGTSILTRVAYGGDP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 SGPQRDALQMGCDILVATPGRILDFIKQGVVETTYVRFVVFDECDRMLDMGFEPQIRDIL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEYQINFHIVNWNLSNPDPTSSEYITLLRDIQDKVTTLYKGSQLHDTFRFCLVTNLTMD- 520
                                                                   :: | |: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 VGPGLDIQQLYWELSQLTHG------VTQLGFYYLDR-DSLFINGYAPQNLSIR 461
                                   -STYQLVDIHVTEMESSVYQP----TSSSSTQHFYLNFT----ITNLPYSQDKAQPGT
                                                                                                                                                                                                                                          GVDSLCNFS-----PLARRVDRVAIYEEFLRMTRNGTQLQNFTLDRS-----SVLVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR.2004 (TrEMBLrel. 26, Created)
01-MAR.2004 (TrEMBLrel. 26, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
GLP 158 79919 77949.
Glardia lambla ATCC 50803.
Eukaryota, Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.6%; Score 143.5; DB 2; Length 6
21.1%; Pred. No. 0.7;
ive 63; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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HSSP; P10081; IFUK.
GO; GO:0005224; F:ATP binding; IEA.
GO; GO:000526; F:ATP-dependent helicase activity; IEA.
GO; GO:000376; F:nucleic acid binding; IEA.
InterPro; IPR001410; DEAD.
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656 AA; 73379 MW; EFF73D219C01978B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7R3F3_GIALA PRELIMINARY;
Q7R3F3;
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Best Local Similarity 21.1%
Matches 114, Conservative
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Pfam; PF00271; Helicas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1790 PSATTRDQIQTESSSQRTISPGETTTSHAPSMSSLAP---STTHM-----LSTTSSS 1838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 HRSSVSTTSTPGTPTV----YLGAS----KTPASIP-----GPSAASHLLILFTLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 RYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGC--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 3443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3443 AA; 365165 MW; 88CC32D3226F632B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.5%; Score 138; DB 2; L 20.8%; Pred. No. 20; ative 92; Mismatches 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50856; AMOP; 1.
PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; AA3 AA, 365165 MW; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 20.8
Matches 182; Conservative
                                InterPro; IPR001846; VWF
Pfam; PF00008; BGF; 1.
Pfam; PF00109; BGF; 1.
Pfam; PF06119; NIDO; 1.
Pfam; PF00194; VWD; 1.
SMART; SM00124; AMOP; 1.
SMART; SM00181; BGF; 1.
SMART; SM00218; NIDO; 1.
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                                                                                       TSI-----PPGNIVINISDISYEYQIEPSSPIIQRRSLSNAVITEVRIANVSALKSA-NR 3933
                                                                                                                                                                                                                                                                      TISSNITNIQFIDALLIATKSANTILANIDETIBYTVLI----QNNGSTT----TNSIFFT 4094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDRDSLFIN------GYAPQNLSIR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARTRVDLLCTYLQPLSGPG-LPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGP
                                                                                                                                                                                                                                                                                                                                                                                     DEPPTTPKPATTFLPPLSEATTAMGYHLKTLTL-----NPTISNLQYSPD--MGKGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFNSTEGVLQHLLRPLFQKSSMGPFYLGCQ-----LISLRPBKDGAATGVDTTCTYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 GEYQINFHIVNWNLS--NPDPTSSEYI-----TLLRDIQDKVTTLYKGSQLHD----TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPCLVTNLTMDSVLVTVKALFSS-NLDPSLVEQVPLDKTLNASFHWLGSTYQLVDIHVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      617 DALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129/SvJ;
MEDLINE=22079426; PubMed=12084055;
Desseyn J.-L., Clavereau I., Laine A.;
"Cloning, chromosomal localization and characterization of the murine mucin gene orthologous to human MUC4.";
Bur. J. Blochem. 289:3150-3159(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Wetazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677 TRNGT-QLQNFTLD------RSSVLVDGYSPNRNEPLTGNSAD 712
                                    LRYMADMGQPGSLKFNITDNVMKHLL---SPLFQRSSLGARYT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
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EMBL; AF520422; AAM66746.1; -; Genomic_DNA.
EMBL; AF520421; AAM66746.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Arsavre.
MGI; MGI:2153525; Muc4.
Ar. Ar.0007160; P:cell-matrix adhesion; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005533; AMOP.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-FEB-2005 (TrEMBLrel. 29,
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QBJZMB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                     TLTLNFTISNLQYSPDMGKGSATFNSTEGVLQH-----LLRPLFQKSSMGPFYLGCQLIS 392
                                                                                                                                                                                                           447 SLF-----INGYAPQNLS-IRG-----EYQINFHIVNWNLSNPDPTSSEYITLLRDIQD 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINES-97313269; Pubmed-9169873;

MEDLINES-97313269; Pubmed-9169873;

Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K., Alemann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M., Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M., Altmann R., Angelo M., Buitrago M.J., Bussereau F., Coster F., Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., Gel Rey F., Doignon F., Domdey H., Dubois B., Fiedler T.A., Fleig U., Floeth M., Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N., Aritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N., Jonniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A., Jonniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A., Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C., Nowee H.-W., Woest D., Nasr F., Nicaud J.-M., Niedenthal R.K., Pandolfo D., Pierard A., Piravandi B., Planta J.L., Rhike M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M., Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhasselt P., Vierndeels F., Vissers S., Voet M., Volckaert G., Wach A., Mambutt R., Wadler H., Zollner A., Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
369 GKFSGEQRRLALYAAMFLPFRKTVYKDTKGKSIPVVNHIFKFSMKRKTSDAETVMNIHQT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Buropean Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
                                                                 393 LRPEKD----GAATGVDTTCTYHPDPVGPGLDIQQLYWELSQL--THGVTQLGFYVLDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=YNRO67C; ORFNames=N3547;
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical 121.1 kDa protein in BIO3-HXT17 intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ensembl; YNR067C; Saccharomyces cerevisiae.
SGD; S0000053SO; DSE4.
GO; GO:0003428; C:cell septum; IDA.
GO; GO:0009277; C:cell wall (sensu Fungi); IDA.
GO; GO:000109; P:cytokinesis, completion of separation; IEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the glycosyl hydrolase 81 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 34, Last sequence update) (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           1117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z71682; CAA96349.1; -; Genomic_DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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GermOnline; 143412; -.
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01-OCT-1996 (
10-MAY-2005 (
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      2094 DTGHSTVITTHGSTLATTQVSLTPSSQNMSTVSMPSTSSQELTSLPQRQHTG--SMETSS 2151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSL-KFNITDNVMKHLLSPLFQRSS- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|| | :: | :: || :: | | : | | : | | SRIPTHKEGTAKDGAFRRDLTINGLPYNINSGAVEDLTERGIDDLKSGKIVTPLPAKATF 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 DLMISGNGPVSAVTYLSDLKLFSVVFALPSSAEPSPPENCGSLSQSYLEAMWSLLKTPRP 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 SQQTHG-----ITRLGPYSLDKDSLYLNGYNEPGPDEP------PTTPKP 317
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EMBL; AF370489; AAX43866.1; "RRNA.

EMBL; AF370489; AAX43866.1; "RRNA.

EMBL; AF370489; Cantochondrion; IDA.

InterPro; IPR012222; PAP CG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W., Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              TRNA adenylyltransferase-like protein.
Name=T22J18.17; Synonyms=At1g22660;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67; Mismatches 185; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     605 AA; 68953 MW; 2DBZ778E49368A18 CRC64;
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Last annotation update)
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PANTHER; PTHR13734; PolyA pol; 1.
Pfam; PF01743; PolyA pol; 1.
PIRSP; PTRSF00814; PolyA pol; 1.
Nucleotidyltransferase; RNA-binding; Transferase.
                                                                                      2152 OPONITPTVVTTSTLLSFSRGSTELÖTMSWGTSS 2185
                                               659 PLARRVDRVAIYEEFLRMTRNGTQLQNFTLDRSS 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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(TrEMBLrel. 29, I
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Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I., Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R., Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C., Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A., Loulseged H., Mungall K., Oliver K., Price C., Quail M.A., Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M., M. Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y., Sharps K., Gibbs R., Loomis W.F., Rosenthal A., Cox B.C., Chisholm R.L., Gibbs R., Loomis W.F., Plazzer M., Kay R.R., Williams G., Dear P.H., Noegel A.A., Barrell B., Kuspa A.; The genome of the social amoeba Dictyostelium discoideum.";
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9497 MW; OCCB0676C5C581FF CRC64;
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InterPro; IPR001611; LRR.
InterPro; IPR001591; LRR.RNinh.
InterPro; IPR003590; LRR_RNinh.sub.
Pfam; PF00560; LRR_1; 2.
PRINTS; PR00019; LECURICHRPT.
SWART; SM00369; LRR_RI; 7.
Hypothetical protein; Leucine-rich repeat; Repeat SEQUENCE 797 AA; 89497 MW; OCCB0676C5C581FF CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQV-----FLDKTLNASFHWLGSTY 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLKSVGLNDRDLWKIFILRDYIYHSSKS-----NTSPTAKDDFELPKDINITP--RNVF 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 RVAIYEEFLRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNSADIQHSGGRSSLEGP 725
                                                                                                                                                                             ---RSSLGARYTG---CRVIALRSVKNGAETRVDLLCTYLQPLSGPGL 269
                                                                                                                                                                                                                                                                                 270 PIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPTTPKPATTFLPPLSEAT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                         KKFWMMSKTFKNDVLKDLNSRLSSKPLLDDKENVSDSYNSFSIRKEQLDSDFENLASKLL 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDVNPMVKISLVNNIMPLCQFF-----GVDKTNDIILPHLITYLNDSNYELRLA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VGPGLDIQQLYWELSQLTHGVTQLG-------FYVLDRDSLFINGYA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        728 EFNALSIYKELL------TŚSIKLLLDPNEWIRQSVICLILAISDNLLDAD 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           937 FEVCYKSEPFSSGSKTAETNF----ESV-----HTLSNSKKDEDSTRGLNSLILP 982
                     SYDKIADALQFNYSNDRNSSLSQNSKFV---PLMLNLKGMPKNYTVKPTVTFMENN--YL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAMGYHLKTL-----TINFTISNLQYSPDMGKGSATFNS------TEGVLQHLL
                                                                                                                       ----QQGSLIILNLIFSLMKSFKQPLSKIKACELIVALSERVNDDCKLDRCLPYLCNLLD
                                                                                                                                                                                                                        EYMDSSSINYQPNNFQTNLSENFTSSSEVACIALTSI-----TTLIMSCSYINPIN----
                                                                                                                                                                                                                                                                                                                                  -----LAACLPYLANVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RPLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTT-----CTYHPDP----
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Name-AAC1; ORFNames-DB0201568;
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TAXID=44689;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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                                                                         ADMGQPGSL-KFNITDNVMKHLLSPLFQ-
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Q54E23;
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DIC 10 5054E2
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Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
Bankler A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
Pilcher K., Chen G., Saunders D., Sodergren B., Davis P.,
Rerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Rarborcher P., Deesny B., Just E., Morio T., Rost R., Churcher C.,
Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
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A Hilliams M.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
Hre genome of the social amoeba Dictyostelium discoideum.";
Nature 0:0.0(2005).
                                  574 KFVDLSFNKINSNFGLDHLVSSLLINHSIHSISLQSNQIDNTSAITLSQLFNSSRQLFSP 633
                                                                            623
                                                                                                                                         RNSS-----IKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMT 677
                                                                                                                                                                                                       RNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNSADIQHSGGRSSLEG-----PRFEQK 730
                                                                                                                                                                                                                                     735 SNDTN-QNDNI-------NNENNLTRISIDL---SSNSPLEVSKVIGLIPRYKSK 778
                                                                                                          634 PKYLNLSGNKIGIGGLKKLINDLSKYSKTHIIYNNNDDNNNNKNENENKSKIK---NLSF
                                                                            ----FTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLF
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1230 AA; 139239 MW; 6F9B094941E6BD2C CRC64;
                ---NASFHWLGSTYQL------VDIHVTEMESSVYQPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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PROSITE; PS50088; ANK REPEAT; 1.
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InterPro; IPR000354; Involucrin rpt.
InterPro; IPR02017; Spectrin.
Pfam; PP00023; Ank; 3
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ORFNames=DDB0184069
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                299 YLNG-----YNEPGPDEPPTTPKPATTFLPPLSEATT-------AMGY 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 HLKTLTLNPTISNLOYSP-DM--GKGSATPNSTEGVLQHLLRPLFQKSSMGPFYLGCQLI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392 SLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQL-----YWELSQLTHGVTQLGFYVLDR 445
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                                                                                                   137 REQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEE----PFTLN 191
                                                                                                                                                                                                                                               251 NNNNNNYSVPNYSP-----VTN--LDHIPSSPLSNNSIPSSPYONPNAPSLQIDEIAM 302
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                                                                                                                                                                                                                                                                                               --SVKNGABITRVDLLCTYLQPLSGPGLPIKQVFHB----LSQQTHGITRLGPYSLDKDSL
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                                                                                                                                                                                                 192 FTINNLRYMADMGQPGSLKFNITDNVMKHL-LSPLFQRSSLGARYTGCRVIALR----
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                                                  218;
       DB 2; Length 1230;
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Bukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
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Last annotation update)
3.3%; Score 131; DB 2; L
1larity 18.5%; Pred. No. 13;
Conservative 96; Mismatches 244;
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Q54JR7_DICDI PRELIMINARY;
Q54JR7;
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ORFNames=DDB0187665;
Dictyostellum discoideum
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Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
Raterbother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
Raterbother H., James K., Quiles M., Mohan M.B., Salto T., Buchrieser C.,
Raterborer A., Felder M., Thangavelu M., Johnson D., Knights A.,
Louiseged H., Mungall K., Oliver K., Price C., Quill M.A.,
Raturaliara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Ray Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
Ray Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
Raturan S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
Rhaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
Rhisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
Milliams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
"The genome of the social amoeba Dictyostelium discoideum.";
"The genome of the social amoeba Dictyostelium discoideum.";
"The genome of the Bequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 HLKTLTLNF-----TISNLQYSPDMGKGSAT-FNSTEGVLQHLLRPLFQKSSMGPFYLGC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 QLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLG----FYVLD 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDSLFINGYAPQNLSIRGEYQINFH-----IVNWNLSNPDPTSSEYITLLRDIQDKVTTL 499
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                                                                                                                                                                                                                                                                                                                                                                 93; Mismatches 206; Indels 234;
                                                                                                                                                                                                                                                                                                                                  Length 1447;
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                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MWPGSRKFNTTERVLQGLL----RPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 PTTSTGVVSEEPF---TLNFT-----INNLRYMADMGQPGSLKFNITD-----
                                                                                                                                                                                                                                                                                                                                                                                                       Torarinsson
                                                                                                                                                                                 Sulfolobus acidocaldarīus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 33909 / NCIB 11770 / DSM 639,
PubMed=15995115, DOI=10.1128/DB.187.14.4992-4999.2005,
Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarin
Greve B., Awayez M., Zibat A., Klenk H.-P., Garrett R.A.,
"The genome of Sulfolobus acidocaldarius, a model organism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.2%; Score 128; DB 2; Length 879; 18.6%; Pred. No. 12;
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EMBL. CP000077; AAY81501.1; -; Genomic_DNA.

Complete proteome; Hypochetical protein.

SEQUENCE 879 AA; 93653 MW; 77081EB79751DCIC CRC64;
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                                                                                 Last sequence update)
Last annotation update)
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879
                                                     Created)
PRT;
                                               13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                           OrderedLocusNames=Saci_2215;
SULAC PRELIMINARY;
                                                                                                                                    Hypothetical protein.
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Matches 152; Conserv
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	-NPDPTSSEYITILIR	Similarity 20.6%; Pred. No. 22; Conservative 120; Mismatches 297; Inde: HRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLMFTI:
Db 488 DSTISSTNIYLSNSVLANQGSSIINCNQNIQSSTVYLTNSQLSSGGSGVANITGTNLYLS 547  Qy 598 QD	#, Created)  4, Last sequence update)  5, Last sequence update)  6, Last annotation update)  12721630; DoI=10.1038/nature01582;  111ales; Bacillaceae; Bacillus;  11ales; Bacillaceae; Bacillus;  12721630; DOI=10.1038/nature01582;  12721630; DOI=10.1038/nature01582;  12721630; DOI=10.1038/nature01582;  12721630; DOI=10.1038/nature01582;  128 A. Reznik G., Mikhailova N., Lapidus A.  109 A. Reznik G., Mikhailova N., Lapidus A.  11 -; Genomic G., Mikhailova N., Lapidus A.  12 -; Genomic DNA.  13 -; Genomic DNA.  14 -; Genomic DNA.  15 -; Genomic DNA.  16 -; Genomic DNA.  17 -; Genomic DNA.  18 Score 128; DB 2; Length 5017;  19 -; Mismatches 327; Indels 212; Gap  127; Mismatches 327; Indels 212; Gap  128 -	3761 SATYQYVSIPTAPPVNRSANSNIVTTSLQNANIISVKSADVNFVSIGQMITYTATLQNIG 156 PYTLD

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                                                                                                                                                                                                                                                                                                                                                                                                                                     SPDMGKGSATFNSTEGVLQHLLRPLFQKSSMGPFYLGC-QLISLRPEKDGAATGVDTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PSLYYTNIDVNSNNSIVTMYPNOVTOYNEFG---FGCPPLFTITINR-----TTDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 YSLDKDSLYLNGYNEPGPDEPPTTPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQY
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                                                                                                                                                                                                                                                                                                        Query Match 3.2%; Score 127; DB 2; Length 1364; Best Local Similarity 21.1%; Pred. No. 28; Matches 114; Conservative 65; Mismatches 190; Indels 172;
                                                                                                                                                                                                                                                              1364 AA; 153737 MW; 3A194428A8D7DD8F CRC64;
                                                                                              Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
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                                                                                                                                 EMBL, AC116984; AAO51340.1; -; Genomic_DNA.
InterPro; IPR006209; EGF_like.
PROSITE; PS01022; EGF_1; UNKNOWN 1.
PROSITE; PS01186; EGF_2; UNKNOWN 1.
HYPOChetical protein.
SEQUENCE 1364 AA; 153737 MW; 3A194428AB
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Q54V40;
  ture 418:79-85(2002)
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ORFNames=DDB0206085;
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NUCLEOTIDE SEQUENCE
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                                                                                                                                                                       241 IALRSVKNGAETRVDLLCTYLQPL--SGPGLPIKQVF-------HELSQQTHGIT 286
                                                                                                                                                                                                                    VVLYML------LLCTLEKLLWFSEPQLPYDDFFSVFAFIICSFVESATSKSTHQKD 286
                                                                                                                                                                                                                                                                                              287 LTNNTQFGKDSVL-----TDKPGTSRK--NDLIPAMASNTDMLVRHLSVVCF---LL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEYO1 --- NF -- HI -- VNWNLSNP --- -- 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : | | : | : | : | : | : | 394 NALNPQHNYNYREEQEKONKQMTYQEIKLSHRIQKSMEALFNIAMFGKSRLQMNAAVL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVKALFSSNLDPSL-----VEQVFLDKTLNASPHWLGSTYQLVDIHVTEMESSVYQPT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSTQH--FYLNFTITULPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDC 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDRSSVLVDGYSPNRNEPLTGNSADIQ-----HSGGRSSLE-----GPRFEQK 730
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VSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHLLSPLF--QRSSLGARYTGCRV
                                                                                                                                                                                                                                                                   287 RLGPYSLDKDSLYLNGYNEPGPDEPPTTPKPATTPLPPLSEATTAMGYHLKTLTLNFTIS
                                                                                                      01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostellum discoldeum (Slime mold). Hypothetical 127.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 MSKTGPKLFEYOKNRPHINGFERVDS-GKLNKAVEGYDRKDVYKNYNRM
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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Q8GAL8;
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Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,

Kerhormou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,

Rarborther P., Desany B., Just E., Morio T., Rost R., Churcher C.,

Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,

Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,

Hauser H., James K., Quiles M., Mohan M.B., Saitor T., Buchrieser C.,

Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,

Loulseged H., Mungall K., Ollver K., Price C., Quail M.A.,

Unushihara H., Herrandez J., Rabbinowitsch E., Steffen D., Sanders M.,

Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,

Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,

Shaulsky G., Schletcher M., Weinstock G., Rosenthal A., Cox B.C.,

Williams J., Dear P.H., Noegel A.A., Barrell B., Kuppa A.,

"The genome of the social amoeba Dictyostelium discoideum.",

Nature 0:0-0(2005).

ENBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 SLQYSNSSFYVTTCSTPYGTGIN-KQPIFQLNSDT------ISDEYS-----YAPPN 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPSITIGNKQCTYIKSNTNELKCKLDPNQNGGKNL-----PVNVNPGGCNSINPHSV 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 KNGAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGP-YSLDKDS---LYLNG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 GKGSATFNSTEGVLQHLLRPLFQKSSMG--PFYLGCQL-ISLRPEKDGAATGVDTTC--- 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 16;
61; Mismatches 151; Indels 141; Gaps
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Pachebat J.A., Gloeckner G., Rajandream M.-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.
EMBL; AAF101000068; EAL67119.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 885 AA; 97603 MW; B19A14755A85D5D8 CRC64;
                     Sucgang R., Berriman M., Song J., Olsen R., Sz
Tunggal B., Kummerfeld S., Madera M., Konforto
Briker A.T., Lehmann R., Hamlin N., Davies R.
Pilcher K., Chen G., Saunders D., Sodergren R.
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21.9%; Pred. No. 16;
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nes 99; Conservative
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Sequence 389, Application US/09404879A

Patent No. 6468546

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C2

CURRENT PILING DATE: 1999-09-44

NUMBER OF SEQ ID NOS: 393

SEQ ID NO SEQ ID NOS: 393

LENGTH: 833
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                                738 LRMTRNGTQLQNFTLDRSSVLVDGYFPNRNBPLTGNS 774
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Fing, Steven P.
APPLICANT: Finger, Gary Richard
APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER;
FILE REFERENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 3.0
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674 LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS
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                                                                                                                                                ; Sequence 389, Application US/09667857; Patent No. 6699664; GENERAL INFORMATION:
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Matches 696; Conservative
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; ORGANISM: Homo sapiens
US-09-667-857-389
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558 DKVTTLYKGSQLHDTFRFCLVTNLTMDSVL/VTVKALFSSNLDPSLVEQVFLDKTLNASFH 617
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APPLICANT: Retter, Marc W.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REPERENCE: 210121.462C6

CURRENT APPLICATION NUMBER: US/09/827,271

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SEQ ID NO 389

LENGTH: 833
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99.9%; Pred. No. 0;
iive 0; Mismatches
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Patent No. 6962980
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696; Conservative
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ORGANISM: Homo sapiens
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                                                                                  NIEDALNOLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSFLARRVDRVAIYEEF
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                                                                                                                                                   LEMIRNGTOLONFILDRSSVLVDGYFPNRNEPLIGNS 774
                                                                                                                                                                                                                                           Sequence 389, Application US/10198053
Patent No. 688870
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
ITILE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAL
FILE REFERENCE: 20121.462C9
CURRENT PILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 389
LENGTH: 833
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; ORGANISM: Homo sapiens
US-10-198-053-389
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; Sequence 312, Application US/09338933
; Patent No. 6488931
; GREEAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: Mitcham, OGNOSTITIONS AND METHODS FOR THE;
; TILLE OF INVENTION: COMPOSTITIONS AND METHODS FOR THE;
; TILLE REPERENCE: 210121.46521
; CURRENT APPLICATION NUMBER: US/09/338,933
; CURRENT PILING DAPE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SEQ ID NO 312
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Best Local Similarity 99.9%;
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ORGANISM: Homo sapien
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF ERQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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          519 PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
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APPLICANT: Bangur, Chaitenya S.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COVARIAN CANCER
FILE REFERENCE: 210121.462C9
CURRENT FALLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 312
LENGTH: 914
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0; Mismatches
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Patent No. 6858710
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Best Local Similarity 99.9%;
Matches 696; Conservative
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; ORGANISM: Homo sapiens
US-10-198-053-312
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APPLICANT: Mitchailow:
APPLICANT: Mitchail Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Red, Steven P.
APPLICANT: Red, Steven P.
APPLICANT: Red, Steven P.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REPREMENCE: 210121.462C5
CURRENT APPLICATION NUMBER: US/09/667,857
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 0;
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Patent No. 6699664
GENERAL INFORMATION:
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ORGANISM: Homo sapien
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                      GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDFTSSEYITLLRDIQ
                                                                                                                                                                                                                                                                                                                           Sequence 312, Application US/09827271
; Sequence 312, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Ranger, Gary W.
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; FILE REPREMENT application 1001-04-04; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT PILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 312
LENGTH: 914
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; Sequence 478, Application US/10198053
; Sequence 478, Application US/10198053
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Hill, Paul
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; TITLE REPERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT PILLING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 478
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ORGANISM: Homo sapiens
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                            VDLLCTYLQPLSGPGLPIKQVPHELSQQTHGITRLGPYSLDKDSLYLNGYNBPGPDEPPT 313
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; Sequence 458, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
GAPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
: APPLICANT: Hill, Paul
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITILE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF OVARIAN CANCER
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
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ORGANISM: Homo sapiens
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; LOCATION: 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,
; LOCATION: 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-198-053-595
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92.5%; Score 3651; DB 2;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches 3;
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Patent No. 6858710
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Retter, Marc W.
APPLICANT: Ranger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CA
FILE REPERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT PILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOOTHWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 595
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ORGANISM: Homo sapiens
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US-10-198-053-595
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                              573 INNLRYWADWGQPGSLKFNITDNVWKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
                                                                  VDLLCTYLQPLSGPGLP1KQVFHELSQQTHG1TRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                  314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
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             INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
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Patent No. 6962880

GENERLI INFORMATION:

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

CURRENT APPLICATION NUMBER: 2001-04-04

NUMBER OF SEQ ID NOS: 461

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SEQ ID NO 458

LENGTH: 1148
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches
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US-09-827-271-458
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Sequence 479.

Batent No. 6858710

GENERAL INFORMATION:

APPLICANT: BANGUR. Chaitanya S.

APPLICANT: Ranger, Gary R.

APPLICANT: FANGER, Marc W.

APPLICANT: Hill, Paul No. 6174 R.

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C9

CURRENT FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 624

SOFTWARE: FASCE FOR Windows Version 4.0

SEQ ID NOS: 624
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ORGANISM: Homo sapiens
US-10-198-053-479
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Sequence 6952980

GENERAL INFORMATION:
APPLICANT: Reter, Marc W.
APPLICANT: Reter, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER;
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER;
TITLE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT PILIG DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SEQ ID NO 459
INDECTH: 1156
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92.3%; Score 3642; D
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches
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CORGANISM: Homo sapiens
US-09-827-271-459
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                                                                                                      VOLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
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APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 459
LENGTH: 1156
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92.3%; Score 3642; D
Best Local Similarity 99.6%; Pred. No. 0;
Matches 694; Conservative 0; Mismatches
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US-10-198-053-459
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US-10-198-053-459
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WLGSTYQLVDIHVTEMESSVYQPISSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
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                  279 GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT
                                                                                 VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                             TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
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GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT
                                                                 INNLRYMADMGOPGSLKFNITDNVMKHLLSPLPQRSSLGARYTGCRVIALRSVKNGAETR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 388, Application US/09667857
; Sequence 388, Application US/09667857
; Retent No. 669964
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Ring, Gordon E.
; APPLICANT: Retter, Marc W.
; APPLICANT: Reter, Marc W.
; APPLICANT: Red, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF CUARRAN CANCER; TITLE OF INVENTION: DIAGNOSIS OF CUARRAN CANCER; TITLE OF INVENTION: DIAGNOSIS OF CUARRAN TAPLICATION NUMBER: US/09/667,857
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT PILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSEQ for Windows Version 3.0
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80.8%; Score 3189; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.8e-282;
Matches 605; Conservative 0; Mismatches 0; Indels
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CRGANISM: Homo sapiens
US-09-667-857-388
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                                                                                                                                                                                 TPKPATTFLPPLSEATTAMGYHLKTLTLNPTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373
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                                                                      INNLRYWADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
                                                                                                                                     GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEBPFTLNFT
                                                                                                                    VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
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                                                    INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
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; Sequence 388, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
    APPLICANT: Mitchan, Jennifer L.
    APPLICANT: King, Gordon E.
    APPLICANT: Algate, Paul A.
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
    FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT PILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 388
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100.0%; Pred. No. 1.8e-282;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 605; Conservative
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ORGANISM: Homo sapiens
US-09-404-879A-388
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US-09-404-879A-388
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219 SRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGBATGVDAICTHRPDPTGP 278
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                                              279 GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSERPFTLNFT
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                       GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGPTHRSSVPTTSTGVVSERPFTLNFT
                                                                                      INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
                                                                                                           339 INNLRYWADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
                                                                                                                                                                                                                                                                                     PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
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Patent No. 6962980

GENERAL INPORMATION:
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C6
CURRENT APPLICATION UNMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 388
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80.8%; Score 3189; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.8e-282;
Matches 605; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-827-271-388
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GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSERFFTLNFT 338
                                                                                                                                    VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT 458
                                                                                                                                                                                                                                                                    TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 518
                                                                                                                                                                                                                                                                                                                                     GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
                                                                                                                                                                                                                                                                                                                                                                                                  613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
                                                                                                                  INNIRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR 253
                                                                                                                                                                                                                                                 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373
                                                                                                                                                                                                                                                                                                                 PLPQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILPTLNFTITNLRYEENMWPG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 SRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP 133
                                                                                                                                                                                 VDLLCTYLQPLSGPGLPIKQVFHBLSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKVTTLYKGSQLHDTPRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 388, Application US/10198053
Facent No. 6888710
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bengur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Panger, Gary R.
APPLICANT: Hill, Paul
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 210121.462C9
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.8%; Score 3189; DB 2; I
100.0%; Pred. No. 1.8e-282;
ive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 605; Conservative
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ORGANISM: Homo sapiens
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US-10-198-053-388
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        QY
        194 INNLRYMADMGQPGSLKFNITDNVMKHLLSPLPQRSSLGARYTGCRVIALRSVKNGAETR 253

        Db
        339 INNLRYMADMGQPGSLKFNITDNVMKHLLSPLPQRSSLGARYTGCRVIALRSVKNGAETR 398

        CY
        254 VDLLCTYLQPLSGPGLPIRQVFHELSQQTHGITRLGPYSLDKDSLYLMGYNEPGPDEPPT 313

        Db
        339 VDLLCTYLQPLSGPGLPIRQVFHELSQQTHGITRLGPYSLDKDSLYLMGYNEPGPDEPPT 458

        CY
        314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373

        Db
        459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 518

        Db
        459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 518

        Db
        459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 518

        Db
        434 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 518

        Db
        519 PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578

        CQ
        434 GVTQLGFYVLDRDSLFINGYAAQNLSIRGEYQINFHIVWMLSNPDPTSSEYTTLLRDIQ

        Db
        579 GVTQLGFYVLDRDSLFINGYAAQNLSIRGEYQINFHIVWMLSNPDPTSSEYTTLLRDIQ

        CQ
        639 DKVTTLYKGSQLHDFRECLYTNLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASFH 698

        CQ
        639 DKVTTLYKGSQLHDFRECLYTNLTMDSVLYTVKALFSSNLDPSLVEQVFLDKTLNASFH 698

        CQ
        614 NIEDA 618

        CQ
        614 NIEDA 618

        CQ
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        CQ
        614 NIEDA 618
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Search completed: March 20, 2006, 07:31:33 Job time : 43.8343 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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Run on:

March 20, 2006, 07:29:34; Search time 27.2939 Seconds (without alignments) 2636.859 Million cell updates/sec

US-10-687-035-1 3945 Title: Perfect score:

1 AAQPARRARRIKIFTHRSSV.....QKLISEEDLNMHTGHHHHHH 748 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	cell surface glyco	probable membrane	fibronectin precur	episialin - mouse	nuclear pore compl	large tegument pro	hypothetical prote		hypothetical prote	DNA-binding protei	cellulose-binding	probable membrane	cell differentiati	carcinoembryonic a	Cf-4A protein - to	outer cell wall pr	hypothetical prote	genome polyprotein	proline-rich pepti				hypothetical prote	membrane protein S	tyrocidine synthet		probable cell surf	hypothetical prote	fibronectin precur
SUMMARIES		H69068	863399	S14428	152257	S42718	T42977	F82884	T41144	T34235	A38926	A44140	F69009	A54280	A35364	T07015	B25039	T17504	JQ1899	A41819	S38156	T11678	AH1115	AH2515	855593	T31075	S45889	AE1717	369	Þ
	£	H69	S63	S14	152	S42	T42	F82	T41	T34	A38	A44	F69	A54	A35	TOT	B25	T17	Š	A41	838	111	AHI	AH2	<b>S</b> 25	T31	845	AE1	T3436	FINHU
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	Length	1408	1117	2477	631	1475	2471	5005	1131	532	1377	1848	1474	888	709	855	1004	1369	3344	5762	838	948	1348	4936	643	3587	919	1622	1777	2386
	Query Match	3.7	3.4	3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	2.9	2.9	2.9	5.9	2.9	2.9	2.9	5.9	2.9	2.9	2.9	2.9	2.9	2.8	2.8	2.8	•	2.8	2.8
	Score	144.5	135.5	123.5	122	121.5	121.5	121.5	121	118	117.5	116	115.5	115	114.5		113.5	113.5	113.5	113.5	112.5	112.5	112.5	112.5	112	112	111.5	111.5	111	111
	Result No.	-	7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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C.Species we Mishbackcerium the farmonicotrophicum C.Date: 05-Dec-1997 #text_change 09-Jul-2004 C.Date: 05-Dec-	103   103
YRLELNSGTDVTIRVLEPDPTITGFNVTPVTGPAPLSYRASLAVTNPHD 865 ITMDSVLVTVKALFSSNLDPSLVEQVFLDKTLANSFHWLG 556  LUIGPTARLAVDGVVVQENIVSLSPGETREIAMGTLLTPGNHTVGINEFSKIVRVLR 922  STYQLVDIHVTEMESSVYQPTSSSTQHFYLNFYITMLPYSQDKAQPGT 605  STYQLVDIHVTEMESSVYQPTSSSTQHFYLNFYITMLPYSQDKAQPGT 605  PASITLSDLRVTPSSGFSPLTITATATATATATATATATATATATATATATATATATAT	313 TTPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVL 368  494 VNPLGIAHVVFSASNPDSSMTMQVDBMTLSSTRVVLSESN 533  369QHLLRPLPQKSSMGPFYLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLY 425  369QHLLRPQKTQLGFYVLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLY 425  360QHLLRPQKTQLGFYVLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLY 425  360QHLLRPQKTQLGFYVLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLY 425  360QHLLRPQKTQLGFYVLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLY 425  360QHLLRPQKTQLGFYVLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLY 425  361QHLLRPQKTQLGFYVLGCQLISLRPBKDGAATGVDTTCTYHPDPVGPGPGLDIQQLY 425  362

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Title: Repeating modular structure of the fibronectin gene: Relationship to protein st:
Reference number: I59049; MUID:86016741; PMID:3863113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :088-references: UNIPARC:UP1000000040C; GB:M11750; NID:g204164; PIDN:AAA41170.1; PID:g
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C, Superfamily: fibromectin; fibromectin type I repeat homology; fibromectin type II repeat C, Superfamily: fibromectin; fibromectin; collagen binding; disulfide bond; duplic C, F,1-32/Domain: signal sequence #status predicted <516.
F,3-3-477/Product: fibromectin great predicted <4M.7.
F,53-88/Domain: fibromectin type I repeat homology <1F2.
F,54-186/Domain: fibromectin type I repeat homology <1F3.
F,187-226/Domain: fibromectin type I repeat homology <1F4.
F,187-226/Domain: fibromectin type I repeat homology <1F5.
F,187-226/Domain: fibromectin type I repeat homology <1F6.
F,187-226/Domain: fibromectin type I repeat homology <1F6.
F,180-401/Domain: fibromectin type II repeat homology <1F7.
F,470-461/Domain: fibromectin type II repeat homology <1F7.
F,510-461/Domain: fibromectin type II repeat homology <1F9.
F,510-508/Domain: fibromectin type I repeat homology <1F9.
F,510-508/Domain: fibromectin type II repeat homology <1F9.
F,510-508/Domain: fibromectin type III repeat homology <1F0.
F,510-508/Domain: fibromectin type
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96-2335/Domain: fibronectin type I repeat homology <1F10>
41-2374/Domain: fibronectin type I repeat homology <1F11>
85-2420/Domain: fibronectin type I repeat homology <1F12>
-79,77-88,98-126,124-136,142-170,168-180,187-216,214-226,232-261,259-271,308-335,333-
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3.1%; Score 123.5; UD 4; Jewston 2017.
Best Local Similarity 19.5%; Pred. No. 14;
Matches 177; Conservative 133; Mismatches 309; Indels 287;
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F;2458/Disulfide bonds: interchain (to 2462) #status predicted
F;2462/Disulfide bonds: interchain (to 2458) #status predicted
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fibronectin type III repeat homology FN3M>
fibronectin type III repeat homology FN3M>
fibronectin type III repeat homology FN3O>
fibronectin type III repeat homology FN3O>
cell attachment (R-G-D) motif
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                                                                                                                          lermatt, E.; Tamkun, J.W.; Hynes, R.O.
.. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
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ibronectin type III
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Residues: 1722-1810 <RES>
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A, Residues: 1-2477 < HYN>
A, Residues: 1-2477 < HYN>
A, Residues: 1-2477 < HYN>
A, Residues: 1-2477 < HYN>
B, Cross-references: UNIPROT: P04937; UNIPARC: UPI000012A7C6; EMBL: X15906; NID: 956163; PIDN R, Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A, Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A, Reference number: S12455; MUID: 88054951; PMID: 2445560
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Residues: 2052-2237 <TAM>

Residues: 3052-2237 <TAM

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A Status: preliminary
A Status: preliminary
A Status: preliminary
A Residues: 1183-1192; GLN', 1268,'P', 1270-1271,'D', 1273,'CF',1276,'PY',1385-1399 <FAL>
A Residues: 1183-1192; GLN', 1268,'P',1270-1271,'D',1273,'CF',1276,'PY',1385-1399 <FAL>
A, Residues: 1183-1192; GLN', 1268,'P',1270-1271,'D',1273,'CF',1276,'PY',1385-1399 <FAL>
A, Cross-references: UNIPARC:UPI0000177AEC; UNIPARC:UPI0000177AEC
A, Cross-references: CAPAMARC:UPI0000177AEC
A, Cross-references: CAPAMARC:UPI000177AEC
A, Cross-references: CAPAMARC:UPI0000177AEC
A, CROSS-REFERENCES:UPI0000177AEC
A, CROSS-REFERENCES:UPI000017AEC
A, CROSS-REFERENCES:UPI000017AEC
A, CROSS-REFERENCES:UPI000017AEC
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Rabo J. 6, 2565-2572, 1987
A;Title: Organization of the fibronectin gene provides evidence for exon shuffling durin
A;Reference number: 800459; MUID:88054950; PMID:3119323
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Cell 35, 421-431, 1983
A;Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
A;Reference number: A27252; MUID:84082067; PMID:6317187
                                                                                                                                                                                                    640 EIDYEVPYDQAAGMYVTNPKIQGVSDGSTATYEPSYTTQGESASGSTMIFALPHHESSFS 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIMODYYTGIQLASTTKGVMGYLTTSLQ----PSTSLNRQISWLPWSSQLGSNLLEYSK 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: :|:: | :| :| :| :| EQLQILLAEVANSELQUSISESISGIAT--YYLGKVIDKYSYILLIVSEIIQDEASTKST- 812
586 YRIT-LLNGVTWL-CYVIGPDDLTSTDF---SLEVSSEYEIKASASVDGLIIQLAVA-PS 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----LVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPY-----SQDXAQPGTTN 607
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A;Cross-references: UNIPARC:UPI000017095C; UNIPARC:UPI0000177AEF; EMBL:X05831
A;Note: the authors translated the codon CCT for residues 51 and 94 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text change 09-Jul-2004 Accession: S14428; S12455; Ā22319; S46203; S00459; A27252; I59049
                                                                                                                                                                                                                                                                                                                                                                                     511 PCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFHWLGSTYQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LENIKSAFDILLON 826
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                                                                                                                          PTSSE--
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1; 557/3; 607/3

Db 843 -	-VYSPSVEGSSTELNLPETANSVTLSDLQPG-VQYNITIYAVE 883	A;Introns: 20/1; 454/3; 472/2; 517/1
Oy 220 -	HILLSPLF-QRSSLGARYTGCRVIALRSVKNGAETRVDLLCT 259	Query Match 3.1%; Scc Best Local Similarity 21.4%; Pro Matches 122; Conservative 55;
260	LPI-KQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEP	89 RP
944	: :     ::   :  :    :   :	Db 58 RPPGDSTS-SPVQSSTSSPATR
Oy 312 -	PTTPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMG- 355	QY 149 HSITELGPYTLDRDSLYVN
Db 1004 F	FVNETDRIVLVTWIPPRARIAGYRLTVGLTRGGQPKQYNVGPMASKYPLRNLQPGSEYTV 1063	Db 110 HGDİSSPATSİSKÖSNSSPVVH
Qy 356 -	KGSATFNSTEGVLQHLLRPLFQKSSMGPFYLGCQLISL 393	
Db 1064 T	PLRS	Db 164 PGD
Qy 394 R	RPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDRD 446	QY 266 GPGLPIKQVFHELSQQTHGI
Db 1119 R	RPSQGGGAPREVTSDSGSIVVSGLTPGVEYTYTIQVLRDGQERD 1162	Db 195 GTSSPATTAPVDSTSSPVAHDD
Oy 447 S	SLFINGYAPQNLSIRGEYQINFHIVNWNLS-NPDPTSSEXITLLRD 491	OY 320 TFLPPLSEATTAMGYHLKT
Db 1163 A	APIVNRVVTPLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQGGTALEE 1222	0I
Oy 492 I	IQDKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLV 539	Qy 366 GVLQHLLRPLFQKSSMGPFYLG
Db 1223 V	/VHADQSSCTFENRNPGLEYNVSVYTVKDDKESAPISDTVIPEVPQLT 1270	Db 307 SVLATTPVYSSM-PF
Qy 540 E	EQVPLDKT-LNASFHWLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTIT 592	Qy 425 YWELSQLTHGVTQLGFYVLDRD
Db 1271 D	:  :    :	DD 347 LGSATSLVYNTSAIATTPVS
Qy 593 N	NLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQVSTF 640	Qy 485 YITLLRDIQDKVTTLYKGSQLH
Db 1326 G	GLEPG-IDYDISVITLINGGESAPTTLTQQTAVPPTTDLRFTNIGPDTMRVTW 1377	Db 389 HSTIASSSYY
Oy 641 R	RSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTRNGTQLQNFTLDRSSVL 694	Qy 545 DKTLNASFHWLGSTYQLVDIHV
Db 1378 A	APPPSIELTNLLVRXSPVKNEEDVAELSISPSDNAVVLTNLLPGTEYLVSVSSV- 1431	Db 415SVGVSF
Qy 695 V	VDGYSPNRNEPLTGNSADIQHSGGRSSLEGPR-FEQKLISEEDLNMHTGH 743	Qy 605 TTNYQRNKRNIEDALNQLFRN-
Db 1432 -	GLDSPTGFDSSDVTANSFTVHWVAPRAPITG	Db 441 SNYYQELKRNISGLFLQIFNGD
Qy 744 -	-нинн 748 	RESULT 5
Db 1481 R	книжн 1486	S42718 nuclear pore complex protein nupl53
RESULT 4		C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revisi
15225/ episialin - mouse		R; McMorrow, 1:; Bastos, R:; Horton,
C; Date: 02-Aug-	-Aug-1996 #text_change 09-Jul-2004	Blochim. Blophys. Acta 1217, 219-223 A;Title: Sequence analysis of a CDNA a.beforence mimber. 542718. MITD:941
C; Accession: I: R; Vos, H.L.; De		A; Accession: S42718
Biochem. Biophy A;Title: The mc A;Reference num	30, 1991 and its promoter. Rapid evolution of the repeti ; PMID:1958179	A;Molecule type: mRNA A;Residues: 1-1475 <mcm> A;Cross-references: UNIPROT:P49790;</mcm>
A;Accession: I: A;Status: preli A;Molecule type A;Residues: 1-6		Query Match Best Local Similarity 19.4%; Pr Matches 86; Conservative 57;
A; Cross-referer	nces: UNIPROT:Q02496; UNIPARC:UPI000002A11B; GB:M77226; NID:g199835; PIDN:	Qy 7 RARRIKLFTHRSSVSTTSTP
A,Status: prel: A,Molecule type	Johnson, translated from GB/EMBL/DDBJ =: mRNA	351
A;Residues: 1-0 A;Cross-referer	531 <re2> nces: UNIPARC:UPI000002A11B; GB:M84683; NID:g199842; PIDN:AAA39756.1; PID:</re2>	Qy 61 ITNLRYEENMWPGS
C;Genetics: , A;Gene: Mucl		DD 395 KINQRIDNKCSIGYEKNMIPGC

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23, 1994
NA encoding a human nuclear pore complex protein, hnup
4154002; PMID:8110839
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Pred. No. 8.1;
; Mismatches 162; Indels 139; Gaps 17;
Score 122, DB 2, Length 631;
red. No. 1.9;
Mismatches 207; Indels 186; Gaps 26;
                                                                                                                                                                                                                                ORSSLGARYTGCRVIALRSVKNGAETRVDLLCTYLOPLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| | ||:
KPVSIATNRSVYFKPSLTPSG-----EFR 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LPA 434
                                                                      RPEKDGEATGVDAICTHRPDPTGPGLDREQLYLELSQLT 148
                                                                                                       | :| :| :
| SPAPEDSTSTAV-LSGTSSPATTAP-----VNSASSPVA 109
                                                                                                                                                   NGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQ 205
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|:|:|||||::|
                                                                                                                                                                                   ITRLGPYSLDKDSLYLNGYNEP----GPDEPPTTPKPAT 319
                                                                                                                                                                                                                                                                                                                                     -----LTLNFTISNLQYSPDMGKGSATFNSTE 365
                                                                                                                                                                                                                                                                                                                                                                                                                  GCQLISLRPEKDGAATGVDTTCTYHPDPVGPG-LDIQQL 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----STTKVTSGSAIIPDHNGSSVLPTSSV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSE 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFL 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - human
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È	113 KDGBATGVDAICTHRPDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHR 172	DD 590 BIBLK-NISSM-FTSBLGEDPSVICTNBEYTALLLAIBNLKBKIPSRKQELHABBIYFQS 647
음 &	435 ANGLSSGVGGGGGKMRRERHAFVASKPLEEEEMEVPVLPKISLPITS 481 173 SSVPTTSTGVVSREPFTINPTINNIRYWADMGOPGSLKFNITDNVWKHILSPLFO 227	Qy 389 QLISLRPEKDGAATGVDTTCTYHPDPVGPG-LDIQQLYWELSQLTHGVTQLGFYVLDRDS 447 :   :   :   :     :   :     :
; <u>8</u>	:   :  :  :  :  :  :  :  :  :  :  :  :	448 LPINGYAPONLSIRGEYOINFHIVNWNLSNPDPTSSEYITLIRDIQDKVTTLYK
È i	RSSLCARYTGCRVIALRSVKNCAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITR	675 VFLEKLKPVEQKLTTBVNELLTDLLHNIKQDATEILPV-PDFTTILKNIQSTLQLLH-
<u>8</u> 8	542 PSSIGFTFSVPVAKTAELSGSSSTLEPIISSSAHHVTT 579	OY 502 GSQLHDTFRPCLVTNITMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFHWLGSTYQL 561
5 A	THE THE THE THE THE THE THE THE THE THE	562 VDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTHYQ
රු සි	PPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLRPLFQKSSMG	749QLSYIGWEVAELSHKÖWNFPPASPIIPLÖLLDBIKTEVQ
8 8	94U FAISLLEGRAVID 0/5 383 PFYLGCQLISLRPEKDGAATGVDT 406	DD 788 RVTAKQTQETLNQILSDVQSILASPARQTSFILQHYITQAGTLVGBSKNETFES 845
අු	676 NKCIACQAAKLSPRDTAKQTGIET 699	OY 660 LARRYDRVALYEEFLRMTRNGTQLONFTLDRSSVLVDGYSPNRNEPL 706
RESULT T42977	9	
Large C; Speci	tegument protein - ateline herpesvirus 3 (strain 73) cies: ateline herpesvirus 3	
C; Date	ecy: Brrain /3 1-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004 ssion: T42977	nypocnetical protein 00459 (imported) - Oreapiasma urealfilicum C;Species: Ureaplasma urealfilcum C.Date: 18-And-2000 #semmence revision 20-And-2000 #text change 20-And-2000
R, Albre	echt, J.C.; Fleckenstein, B.	C. Accession: F82884 R.Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H.
A; Refer A; Refer	Tiption: Primary structure of the herpesvirus ateles genome. rence number: 222274 Raiton: T42977	submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini A:Reference number: A82870
A;Stati A;Molec	us: preliminary, translated from GB/EMBL/DDBJ	A;Accession: P82884 A;Status: preliminary
A;Resid A;Cross A;Exper	A;Residues: 1-24/1 cALBA. A;Cross-treferences: UNIPROT:Q9YTK3; UNIPARC:UPI00000EFC9B; EMBL:AF083424; PIDN:AAC95588. A;Experimental source: strain 73	Molecule type; Residues: 1-5; Cross-referer
Quer) Best Match	Query Match 3.1%; Score 121.5; DB 2; Length 2471; Best Local Similarity 18.1%; Pred. No. 19; Matches 139; Conservative 123; Mismatches 279; Indels 229; Gaps 34;	A Experimental source: serovar 3; blovar 1 C;Genetics: A;Gene: UU495 A;Genetic code: SGC3
& a	1 AAQPARARRIKLFTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFT 60 :::  ::  :	Query Match 3.1%; Score 121.5; DB 2; Length 5005; Best Local Similarity 19.6%; Pred. No. 58; Matches 135; Conservative 108; Mismatches 216; Indels 229; Gaps 39;
දු දු	61 ITNLRYEENMWPGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATG- 119 	OY 136 DREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVS-EEPFTLNFTI 194 :     :     : :     : :     ::       ::   ::     ::   ::     ::   ::   ::     ::   ::     ::   ::     ::   ::     ::   ::   ::     ::   ::   ::     ::
È	VDAICT-HRPDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYV	PGSLKFNITD-NVMKHLLSPLFQRSSLGAR
d d		NLMNEYYLKLKYI DNNGDVVWSDPVSI NNVNNEYEFNLPDKNALKSNRI YK
දු දු	167 NGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHLLSP 224	OY 235 YTGCRVIA-LRSVKNGAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSL 293
දු දු	225 LFQRSSLGARYTGCRVIALRSVKNGAETRVDLLCTYLQPLSGPGLPIKQVFHE 277	OY 294 DKDSLYLNGYNEPGPDEPPTTPKPATTFLPPLSBATTAMGYHLKTLTLN 342
È	278 LSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPTTPKPATTFLPPLSEATTAMGYHLK 337	
q <sub>Q</sub>		884 FT-SNLEYD-DITKTWGVKIHANNLSPEVNYQIKSVKFRQKPVLGAFNNN
à	338 TLTLNPTISNLQYSPDMGKGSATFNSTEGVLQHLLRPLFOKSSMGPFYLGC 388	OY 391 ISLRPEKDGAATGVDTTCTYHPDPVGFGLDIQQLYMELSQLTHGVTQLGFYVL 443

DD 444 DRDSLFINGYAPQNLSIRGEYQINFHIVNMNLSNPD	Qy 179 STGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQR 228
RESULT 8  141144  hypothetical serine rich protein - fission yeast (Schizosaccharomyces pombe)  Cispecies: Schizosaccharomyces pombe  Cispecies: Schizosaccharomyces pombe  Cispecies: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004  Cispecies: O1-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004  Cispecies: D1-10-10-10-10-10-10-10-10-10-10-10-10-10	STATEMENTALE
A;Cross-references: UNIPARC: UP10000161F34; EMBL:AL031543; NID:94239667; PIDN:CAA20837.1; A;Cross-references: UNIPARC: UP10000161F34; EMBL:AL031543; NID:94239667; PIDN:CAA20837.1; A;Experimental source: strain 972h-; cosmid c74 C;Comment: For a possible alternative initiator product, see PIR:T42367. C;Gonectics: A;Genetics: A;Ge	RESULT 9 T34235 hypothetical protein F22A3.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T34235 A;Becented to the EMBL Data Library, November 1995 A;Reference number: Z21492 A;Reference number: Z21492 A;Reference number: Z21492 A;Reference prollinary; translated from GB/EMBL/DDBJ A;Residues: 1-532 cHAL> A;Residues: 1-532 cHAL> A;Residues: 1-532 cHAL> A;Residues: 1-532 cHAL> A;Residues: S5/1; 71/1; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 331/3; 357/1; 391/1; 511 A;Introns: S5/1; 71/1; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 331/3; 357/1; 391/1; 511 A;Introns: S5/1; 71/2; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 31/3; 357/1; 391/1; 511 B;Introns: S5/1; 71/2; 99/1; 148/3; 176/3; 190/1; 239/1; 303/1; 31/3; 357/1; 391/1; 511 A;Introns: S5/1; 71/2; 99/1; 148/3; 176/3; 190/1; 219/1; 118; DB 2; Length 532; Best Local Similarity 20.5%; Pred. No. 2.7; Best Local Similarity 20.5%; Pred. No. 2.7; Matches 101; Conservative 59; Mismatches 171; Indels 162; Gaps 25;

È	255 DLLC-TYLQPLSGPGLPIKQVPHELSQQTHGITRLGPYSLDKDSLYLNGYNEP 306	)£7 da	:  :     :
qq	9 DFLCSTCMSTWSGIRKKQASPGIESRESVFGLKRVCAVAARRAP52	0,7	270 PIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPTTPKPATTFLPPLSEAT 329
ò	307 GPDEPPTTFKPATTFLPPLSEATTAMGYHLKTLTLNFIISNLQYSPDMGKGSATF 361	Db 765	5SNRTFGISELNQRITELKMEPGTDAEIKIPKLPNTTIGGISEDP 808
qq	53 -PPEPPPPPPPPTPTLLFKLSETQFHGLNGFAFPFNNLEYKYGSCKSDDSSSM 103	Qy 330	D TAMGYHLKTLTLNPTISNLQYSPDMGKGSATFNSTEGVLQHLLRPLRPQKSSMGPFYLGCQ 389
È	362 NSTEGVLOHLIRPLPQKSSMGPFYLGCQLISLRPEKDGAATGVDT 406	908 qq	809 LQNQTSFRNTVSNKQGTVSGSIQGQFRRDSQNSTASTYKGSMQ 851
ą	104 NGT-GSVGHRWNSLSPEPHSGTESTASTPFVKSEF-PFDDDLFGIDQ 148	Qy 390	LISLRPBKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQ
ò	407 TCTYHDDPVGPGLDIQQLYWELSQLTHGVTQLGFPVVLDRD-SLFINGYAPQNLSIRGE 463	Db 852	: :     : :     : :     : :     :     :     : :     : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : : :     : :     : : :   :
g	149 VNNVKPHPMDMPCNLPIQPIEYNRRFSKDADHSTFVKNEIEENI 192	Oy 435	S VTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYI-TL 488
ò	464 YQINFHIVNWNLSNPDPTSSEYITLIRDIQDKVTTLYKGSQLHDTF 509	Db 904	TSTSGLPVLNKESNKSLNACINKPNIG
g	193 LNFN-VNPBIAQDNGLDTQQIDIYRDILLRHLIQDISTTCAKLGLPNDFYLWSSEHGA 249	Qy 489	IRDIQDKVTTLYKGSQ 504
š	510RFCLVINLTMDSVLVIVIVALFSSNLD 535	Db 954	-14
<del>Q</del>	250 RWINEMCMQFNLQPPRNCSITGIDLLGMSQKDFEMILPAGGDTLHAQLQVWKTAFENYHP 309	Qy 505	S LHDTFRPCLV
ò	536 PSLVEQVFLDKTLNASFHWLGST-YQLVDIHVTEMESSVYQPTSSSSTQHF 585	Db 1014	1014 LDPLTNISRESTTPHSFDINVGKTNNIASLINKDNLFKDLFTVSIKADMAMTSDQHPNER 1073
qq	310 PVTVQSSGMTAAENNMQSKTNWLASTNNQTNNMAAAENPNHPFFNGNGGYPNMSMSSF 367	Qy 542	VFLDKTLNASFHWLGSTYQLVDIHVTB-MESSVYQPTSSSSTQ 583
ઠે	586 YLNPTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQVSTFRSVPN 645	Db 1074	INLDEVEBLILPDEMLQYLNLVKDDTNHLEKEHQAVPVGSNVSETIAS
QQ Op	368 PQCGTVLPSPSNSDTSSNGSSQ-DWADDDIDLAMNNSNCGFSNFFHNQG 415	Qy 584	H HFYLNFIITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYFSDCQVSTFRSV 643
È	646 RHHTGVDSLCNPS 658	Db 1131	- YYTNKQILTPPSNVD-IQPNTTFTVQDKFAMTAVGGSFSQRELSTL-AV 1177
đ	416 YMNSPIDAMCNGS 428	Qy 644	PIRH-HIGVDSLCNFSPLARRVDSVAIYBEFLRMTRNGTQLQNFTLDRSS 692
RESULT 10	10	da .	3 PNEHGHAKCESFHHQSQKYMNTDIGSKQQSALPSAHQRQTEKSNYNQIIDSSMTSLPB 1235
A38926	A38926 DNA-hinding protein ci (D) - fruit fly (Drosophila melanomaster)	Фу. 693	S VLVDGYSPNRNE 704
C; Spec. C; Date	a melan #sequen	Db 1236	1236 INVDSIYP-RNB 1246
C; Acce R; Slus	ssion: A38926; A35817; S12122; S12769 rski, D.	RESULT 11	
Submit: A, Refer	ed to GenBank, October 1990 ence number: A38926	A44140 cellulose-bir	nding protein A precursor - Clostridium cellulovorans
A; Accel A; Molec	nsion: A38926 ule type: mRNA	C;Species: C] C;Date: 27-Ju	. change 09-Ju
A; Resi	lues: 1-1377 <slu></slu>	C; Accession: R:Shosevov. C	A44140 J.: Takadi, M.: Goldstein, M.A.: Doi. R.H.
R;Oren. Genes I		Proc. Natl. A	Proc. Natl. Acad. Sci. U.S.A. 89, 3483-3487, 1992 A, Title: Primary sequence analysis of Clostridium cellulovorans cellulose binding proteir
A;Titl A;Refer	A,Title: Cloning and characterization of the segment polarity gene Cubitus interruptus d A,Reference number: A35817; MUID:90346286; PMID:2166702	A; Reference no A; Accession: 1	number: A44140, MUID:92228810, PMID:1565642 A44140
A; Acce A; Molec	ssion: A35817 ule type: mRNA	Sta Mol	rus: preliminary ecule type: genomic RNA
A;Residues: A;Cross-refe	Residues: 'MKISFITRSIQKILTCL',114-1151,'K',1152-1377 <ore> Cross-references: UNIPARC:UP1000017BE89; GB:X54360</ore>		Residues: 1-1848 <sho> Cross-references: UNIPROT:P38058; UNIPARC:UPI00001271C5; GB:M73817; NID:9144748; PIDN:</sho>
C;Gene A;Gene	ics: : PlyBase:ci	C,Genetics: A,Gene: cbpA	
A; Cros C; Keyw	Cross-references: Flybase:FBgn0004859 Keywords: DNA binding; zinc finger	Query Match	Query Match 2.9%; Score 116; DB 2; Length 1848;
Query	Mat	Matches 13	vat
Matches	132; Conservative	9,	14 FTHRSSVSTTSTPGTPTVXLGASKTPASIFGPSAAS 49
ò	166 VNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSL 209	Db 154	I YTOTNDYSFDASSSTPVVNPKVTGYIGGAKVLGTAPGPDVPSSIINPTSATFDKNVTKQA 213
셤	675 VNGVRASDSLLTYSPDDLAENINLDDGWNCDDDVDVADLFIVLRAWVNIGNGNAS 729	ογ 20	50 HILILFTINFTITNLRYBENMWPGSRKFNTTBRVLQGLLRPLFKNTSVGFLY 101 :
È	210 KFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETRVDLLCTYLQPLSGPGL 269	. Db 214	214 DVKTTWTLNGNTFKTITDANGTALNASTDYSVSGNDVTISKAYLAKQSVGTTT 266

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                                                                                                                                                                                                                                                                                                                                       QLSFDATLLEVVSITAGDIVLNPSVNFSSVVNGSTIKLLFLDDTLGSQLISKDGVFATIN 760
                                                                     -----VNGFTHR-SSVPTTSTGVV----SEEPFTLNFTINNLRYMADMGQPGSLKFN 212
                                                                                                                                                                             PITPKPATIFLPPLSEATIAMGYHLKTLILNFIISNLQYSPDMGKGSAIFNSTEGVLQHL 371
                                                                                                                                                                                            --------AAGSVTINIGDPILEPT 580
                                                                                                                                                                                                              LRPL---FOKSSMGPFYLGCQLISLRPEXDGAATGVDTTCTYHPDPVGPGLDIQQLYWEL 428
                LNFNFSAGNPOKLVITVVDTPVEAVTATIGKVQVNAGETVAVPVNLTKVP---AAGLATI 323
                                                                                                                                          ----GP----GLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEP 311
--DGEATGVDAICTHRPDPTGPGLDRE
                                                                                                       213 ITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKN----GAETRVDLLCTYLQPLS---
                                                                                                                                                    SQLTHGVTQLGFYVLDRDSLFINGYAPQNLS--IRGEYQINFHIV-
                                                                                                                                                                                                                           384 ITFKAKAITGTTAKVTSVKLAGTPVVGDAQLQEKPCAVN---
                                                                                                                                                                                                                                                                                   --NWNLSNPDPT-SSBYITLLRDIQDKVT----TLYKG-
                                                                                                                                                                                                                                                                                                                                                                     FKAKSVTSTVTTPVKVSGTPVF-ADGTLAELSY 792
                                                                                                                                                                                                                                                                                                                                                          564 IHVTEMESSVYOPTSSSSTOHFYLNFTITNLPY 596
                                                                                                                                                                                              STVTTPVTVSGTPVFADGTLAEVQSKT-
SGCRLTLLRPEK--
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probable membrane protein MTH1074 - Methanobacterium thermoautotrophicum (strain Delta H probable membrane protein MTH1074 - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004 C;Accession: F69009 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004 C;Accession: F69009 Methanobacterium thermoautotrophicum July Aldredge, T.; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Recence number: A69000; MUID:98037514; PMID:9371463 A;Accession: F69009 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Mesidues: 1-1474 <ATH>A;Accession: F69009 A;Status: Draw A;Accession: 1-1474 <ATH>A;Accession: C;Acoss-references: UNIPROT:027146; UNIPARC:UPI0000666BF; GB:AE000878; GB:AE000666; NIE A;Genetics: Milloration C;Keywords: duplication

⋧ 원

38; 215; Indels 1 2.9%; Score 115.5; DB 2; Similarity 20.5%; Pred. No. 21; Bs. Conservative 92; Mismatches 306; Matches 158; Query Match Best Local

878 622 930 682 977 --SVTGNERDPDRTNNDAVSTLNAVSADLS-----IQKTVD-------RPVINN 735 GETATFTVIVRNAGPDTPSNVVSDLLPAGLSIISYTVTQGSFNTTTGVWEVGSLPALFQ 795 853 539 GSYYMGTWNVGTLNYLBIATLTIIARVNATGSLTNFANIT-----SPNFDPNPDNNN 590 THGITRLGPYSLDKDSLYLNGYNEPGPDEPPTTPKPATTFLPPLSEATTAMGYHLKTLTL 341 NFTISNLQYSPDMGKGSA--TFNSTEGVLQHLLRPLFQKSSMGPFYLGCQLISLRPEKDG 399 400 AATGVDTTCTYHPDPVGPGLDI--QQLYWELSQLTHGVTQLGFY----VLDRDSLFINGY 453 LGARYTGCRVIALRSVKNGABTRVD-----LLCTYLQPLSGPGLPIKQVFHE-LSQQ 281 AILTLVVRATQAGFQTN--IVNVSSELPDPLPGDNVDAVTVDVRPSADVKITKTVSNTAP 931 INTVSVISTEXDPDLT-----NHAAG---LLN----AEAVADIAVQKTVLLTFINNGQ -----SVNNPEPY-VGENIQYTITVSNRG--PDNAAGVVVEDVLPAGLIPISATPSK 504 QLHDTFRFCL-VINLIMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFHWLGSTYQLV DIHVTEMESSVYOPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKRNIBDALNQL DTAEVVGIPVADLLIVKOVSDPRPDYGSVVTFTVAVTNLGPSNATGVTVTDILSPGLVYL APONLSIRGE---YOINFHIVNWNLSNPDPTSSEYITLL-----RDIQDKVTTLYKGS FRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTRNGTQ LOGILRPLFKNTSVGPLYSGCRLT--LLRPEKDGEATGVDAICTHRPDPTGPGLDREQLY -----TINF-TINNLRYMADMGQPGSLK--FNITDNVMKHLLSPLF----ORSS -----RT-----: | | | : : | | : | | | ITNFT-----VITINNGPN---DATGVAVIDILPPGLGLLSHSASQGTFAG 1020 LONFILDRSSVLVDGYSPNRNEPLIGNSAD------IQHSGGRSSLEG 724 LELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPF-854 DFGDTVVFYITVTNLGPDTATVV----84 142 231 591 342 969 454 964 683 393 448 490 282

NiAlternate names: loose aggregate C
C;Species: DictyOstellium discoideum
C;Species: DictyOstellium discoideum
C;Species: O9-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004
C;Accession: A54280
R;Dynes, J.L.; Clark, A.M.; Shaulsky, G.; Kuspa, A.; Loomis, W.F.; Firtel, R.A.
A;Title: LagC is required for cell-cell interactions that are essential for cell-type of A;Reference number: A54280
A;Accession: A54280
A;Accession: A54280
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA (Dictyostelium discoideum) cell differentiation protein LagC precursor - slime mold

dif

GB:U09478; NID:g495172; PIDN:1 A;Residues: 1-888 <DYN>
A;Cross-references: UNIPROT:P42523; UNIPARC:UPI000012E1FF;
A;Note: authors translated the codon TCA for residue 34 as C; Genetics:

A;Gene: lagC C;Superfamily: Dictyostelium discoideum cell differentiation protein LagC C;Keywords: transmembrane protein 83

Length 1474;

26 PGTPT-VYLGASKTPASIFGPSAASHLLILFTLN-FTITNLRYEENMWPGSRKFNTTERV

preliminary

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47;
                                                                 398
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                                                                                                                                                                                                                                                        ---ELSQQTHGI---- 285
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                                                                                                                                                                                                                                                                                                       TRIGBYSLDKDSLYLNG-----YNEPGPDEPPTTPKPATTFLPPLSEAT----TAM 332
                                                                                                                                                                                                                                                                                                                               ----KSVTFELPHLRCRSFNINFTRS 453
                                                                                                                                                                                                                                                                                                                                                       GYHLKTLTLNFTIS-NLQYSPDMGKGSATFNSTEGVLQHLLRPLFQKSSMGPFYLGCQLI 391
                                                                                                                                                                                                                                                                                                                                                                       SLRPE------KDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQ 437
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                                                                                                                                                                    SPDGI--DQP---NFIISVNHKQIQNNYNRV----DPGPMSVNITVDEVSIEKNYIHCF
                                                                                                                                                                                                                                                                             ----ANELGGKNLPVNVNFGGCDSTSPNGVSFTYNIPTLSRGSYSNGIVTLIG
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                                                                                                                                                     ------LSPLFQRSSLGARYTGCRVIALRSVKNG
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                           Gaps
                           Indels 298;
   Length 888;
                                                                                                   -----RDSLYVNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           438 LGFYVLDRDSLFINGYAP---QNLSIRGE-YQINFHIVNWNLS-
Query Match
2.9%; Score 115; DB 2; L
Best Local Similarity 19.6%; Pred. No. 10;
Matches 157; Conservative 109; Mismatches 235;
                                                   -----VDAICTHRP-
                                                                                                  REQLYLELSQLTHSITELG----PYTLD-----
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NVTIEEIKL----SPSPN 835
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                                                   RPEKDGE---ATG----
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344 LECKLD-
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C;Accession: T07015
R;Takken, F.L.; Schipper, D.; Nijkamp, H.J.; Hill, J.
Plant J. 14, 401-411, 1998
A;Title: Identification and Ds-tagged isolation of a new gene at the Cf-4 locus of tomato T07015 Cf-4A protein - tomato C;Species: Lycopersicon esculentum (tomato) C;Date: 30-Apr\_1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004 613 RESULT 15 antig carcinoembryonic 09-Jul-2004 for a rat Species: Rattus norvegicus (Norvay rat) A35364
carcinoembryonic antigen-related protein (clone rnCGM1) - rat carcinoembryonic antigen-related protein (clone rnCGM1) - rat C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Aug-1990 #sequence\_revision 17-Aug-1990 #text\_chang C;Accession: A35364
R;Rebsstock, S.; Lucas, K.; Thompson, J.A.; Zimmermann, W. J. Biol. Chem. 265, 7872-7879, 1990
A;Title: cDNA and gene analyses imply a novel structure for a A;Reference number: A35364; MUID:90243655; PMID:2335509
A;Accession: A35364

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A Molecule type: mRNA
A; Residues: 1-709 <REB>
A; Cross-references: UNIPROT: 063111; UNIPARC: UPI00000E81AF; GB: M32474; NID: 9203430; PIDN: A; Cross-references: UNIPROT: 063111; UNIPARC: UPI0000E81AF; GB: M32474; NID: 9203430; PIDN: A; Cross-refamily: carcinoembryonic antigen recursor amino-terminal homology <CEA1> F; 1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2> F; 242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2> F; 480-612/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA3> F; 633-690/Domain: immunoglobulin homology <INM2>
                                                                                                                                                                                                                                                                   30
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                                                                                                                                                                                                                      Match 2.9%; Score 114.5; DB 2; Local Similarity 20.0%; Pred. No. 7.6; es 136; Conservative 80; Mismatches 263;
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A;Reference number: 215863; MUID:98335213; PMID:9670557
A;Accession: T07015
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-855 <-TAK>
A;Cross-references: UNIPROT:050024; UNIPARC:UPI00009FC28; EMBL:Y12640; NID:e1289424;
A;Experimental source: strain Cf-4; isolate MM-Cf-4
A;Genetics
A;Genetics
A;Map position: 1
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                                                                                                                                                                                                                                   VGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDFTGPGLDREQLYLELSQLTHSITELGP 156
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B25039
outer cell wall protein precursor - Bacillus brevis (strain 47)
N;Alternate names: S-layer protein OWP
C;Species: Bacillus brevis
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llarity 19.6%; Pred. No. 12;
Conservative 111; Mismatches 209;
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                                                                                                                                      Query Match
Best Local Similarity
Matches 149; Conserv
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C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C;Accession: B25039; B28555
R;Tsuboi, A.; Uchihi, R.; Tabata, R.; Takahashi, Y.; Hashiba, H.; Sasaki, T.; Yamagata, I
J. Bacteriol. 168, 365-37, 1986
A;Title: Characterization of the genes coding for two major cell wall proteins from proteins A;Reference number: A91824; MUID:87008404; PMID:2428810
A;Accession: B25039
A;Molecule type: DNA
A;Residues: 1-1004 <TSU>A;Accession: B25038
A;Molecule type: DNA
A;Residues: 1-1004 <TSU>A;Adachi, T.; Sasaki, T.; Hayakawa, S.; Yamagata, H.; Tsukagoshi, R;Tsuboi, A.; Uchihi, R.; Adachi, T.; Sasaki, T.; Hayakawa, S.; Yamagata, H.; Tsukagoshi, J. Bacteriol. 170, 935-945, 1988
A;Title: Characterization of the genes for the hexagonally arranged surface layer protein A;Reference number: A91893; MUID:88115203; PMID:2828336
                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: B28555
A;Molecule type: DNA
A;Residues: 1-65 - CIS2-
A;Residues: 1-65 - CIS2-
A;Cross-references: UNIPARC:UP1000016E6A4; GB:M19115; NID:g143548; PIDN:AAA22761.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 IKQVFHELSQQTHGIT-----RLGPYSLDKDSLYLNGYNEPGPDEPPTTPKPATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 YVASVODSDFRIEGYTIAGVETKGEVVTIKVTELDIDDSDATPTVAVIGSVEDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::: ||| |---EPQKAIDGVSAPDKEAPVVTGVEAGKTYNTAVTPDSADKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        898 TVKFKVDIPAEDKKAPEIKTVTDDKVAVADAPKWEAPKATATDDVD--GDISDK1AVTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TGVV/SEEPFTLNFTINNLRYMADMGQPGS---LKFNITDNVMKHLLSPLFQRSSLGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GCRVIALRSVKNGA---ETRVDLLCTYLOPLSGPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPPLS-----EATTAMGYHLKTLTLNFTISNLQY-SPDMGKGSATFNSTEGVLOHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 PLFQKSSMGPFYLGCQLISLRPEK--DGAA------TGVDTTCTYHP--DPVGPGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PKNTSVGPLYSGCRLTLLRPEKDG-----EATGVDAICTHRP-----DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGPGLDRRQLYLELSQLTHSITE-LGPYTLDRDSLYV-NGFTHRSSVPTTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPGSRKFNTTBRVLQGLLRPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Start codon: GTG
C;Keywords: cell wall
F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%; Score 113.5; DB 2;
18.9%; Pred. No. 16;
tive 88; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------------X
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Best Local Similarity 18.9
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GSQLHD 507
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Genome polyprotein - papaya ringspot virus
NiConcains: 46K protein; 63K protein; 6K protein; coat protein; cylindrical inclusion pro
Cispecies: papaya ringspot virus, PRSV
Cispecies: papaya ringspot virus, PRSV
Cispecies: papaya ringspot virus, PRSV
Cispecies: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 09-Jul-2004
Cispecies: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 09-Jul-2004
Cispecies: No.10199; PQ0509; No.10199; No.10199; No.10199; No.10199; No.10199; No.10199; PMID:1402799
A; Title: Complete nucleotide sequence and genetic organization of papaya ringspot virus F
A; Reference number: JQ1899; MUID:93019006; PMID:1402799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: genomic RNA
Residues: 1-3344 <YEH1>
Cross-references: UNIPROT:Q01901; UNIPARC:UPI0000131E61; GB:S46722; NID:g258106; PIDN:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **Reperimental source: type P, strain HA

Superfamily: tobacco etch virus genome polyprotein

Superfamily: tobacco etch virus genome polyprotein

1.547 Product: 63K protein #status predicted orRO>

548-1004/Product: 63K protein #status predicted orRO>

548-1004/Product: 65K protein #status predicted orRO>

548-1004/Product: 46K protein #status predicted orRO>

1402-2036/Product: 46K protein #status predicted orRO>

1402-2036/Product: cylindrical inclusion protein #status predicted ocTP>

1486-1493/Region: nucleotide-binding motif B (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: genomic RNA
Residues: 2561-3344 <WAN>
Cross-references: UNIPARC:UP10000170FCB; EMBL:X67672; NID:g62378; PIDN:CAA47904.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: Nucleotide sequence comparison of the 3'-terminal regions of severe, mild, Reference number: A56603; MUID:9309098; PMID:1456896
                                                            994 PILEATDV-NFTQD---ALVAGELITQN--FYGNITSANI---GSRITIGNANVTQTNIT 1044
          733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : : | : : | : : : | : : | : : | : : : | : : | : : : | : : | : : : | : : : | : : 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676 MTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGN--SADIQHSGGRSSLEGPRFEQKLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SSLGARYTGCRVIALRSVKNGARTRVDLLCTYLQPLSGPGLPIKQVFHELSQQT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 VPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 229; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2094.2520/Product: nuclear inclusion a protein #status predicted <NIA> 7.5221-3037/Product: nuclear inclusion b protein #status predicted <NIB> 3.938-3344/Product: coat protein #status predicted <COP> 7.256/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: protein
Residues: 548-554;1402-1410 <YEH2>
Cross-references: UNIFARC:UPI000017874F; UNIPARC:UPI0000178750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 093/Product: 6K protein #status predicted <PRI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , C.H.; Yeh, S.D.
Virol. 127, 345-354, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITNLRYBENM--WPGSRKFNTTERVLQGLLRPLFKNTSV--GPLYSGCRLTLLRPEKDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 AVGNLISADNTSEFANITSFTTNGLVVNGNIIAAIGNGNVFLANVITANSLTL----QSS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PDPTGPGLDREQLYLELSQLTHSITELGPYTLD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FILINNLRYMADM 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                hypothetical protein A14R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ISSDISNISITGNTSGNVP---AANIATIGTLNTANVVANLVASNVMNAWVTSNIRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.9%; Score 113.5; DB 2; Length 1369; Best Local Similarity 21.3%; Pred. No. 26; Matches 179; Conservative 116; Mismatches 352; Indels 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q89349; UNIPARC:UP100000F912E; E
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Gene: A14R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 RDSLYVN-----GFTHRSSVPTTSTGVVSEEPFTLN----
                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T17504
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LF--OKSSMGPFYLG----CQLISLRPEKDG-
                                                                                                                                                                               C, Accession: T17504
R, Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A, Reference number: Z18806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-1369 <GRA>
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A,Molecule type: protein.
A,Rolecule type: Drotein.
A,Rosidues: 2822-2859 < PE2.
A,Rosidues: 2822-2859 < PE2.
A,Cross-references: UNIPARC:UPI0000179214
A,Cross-references: UNIPARC:UPI0000179214
A,Note: this peptide, designated proline-rich polypeptide IV, can be found at several loc C,Genetics:
B, Septimetics: #status absent
A,Introns: #status absent
A,Note: single copy gene with no introns
C,Reywords: prostatic tandem repeat
C,Reywords: prostatic tandem repeat
F;1-26.Domain: signal sequence #status predicted <NA7
F;27-5761/Product: prostatic proline-rich peptides 637K proprotein #status predicted <NA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YXR079c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S38156
C;Accession: S38156
C;Accession: S38156
S;Pohl, F.M.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
A;Accession: S38184
A;Accession: S38184
A;Accession: S38184
A;Accession: S388 cPOH>
A;Accession: S388 cPOH>
A;Accession: S388 cPOH>
A;Cross-references: UNIPROT:P36159; UNIPARC:UPI0000052ED3; EMBL:Z28304; NID:g486556; PIIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 YSPDMGKGSATFNST------BGVLOHLLRP-LFOKSSMGPFYLGCQLIS---- 392
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                                                                                                                                                                                                                                                                                                                              111 PEKDGEATGVDAICTHRPD------PT-----GPGLDREQLYLELS---QLTH 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 PIKQVFHBLSQQTHGITRLGPYSLDKDSLYLNGYNBPGPDEPPTT-----PKP
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                                                                                                                                                                                                                                          2.9%; Score 113.5; DB 2;
19.8%; Pred. No. 2.6e+02;
tive 79; Mismatches 224;
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Matches 125; Conservative
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A; Molecule type: DNA; mRNA
A; Residues: 1.3706.71',3708-4077,'F',4079-4155,'S',4157-5761 < DE2>
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A; Reperimental source: ventrated
A; Note: sequence extracted from NCBI backbone (NCBIN:100347, NCBIP:100348)
A; Note: sequence extracted from NCBI backbone (NCBIN:100347, NCBIP:100348)
A; Reference number: A41819
A; Reference number: A41819
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A; Molecule type: DNA
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A; Cross-references: UNIPARC: UPI000017CF38
A; Cross-references: UNIPARC: UPI000017CF38
A; Cross-references: UNIPARC: UPI000017CF38
A; Cross-reference number: A13159-13165, 1988
A; Title: A single 12.5-kilobase androgen-regulated mRNA encoding multiple proline-rich E
A; Reservence number: A31966; MUID: 89066721; PMID: 3198617
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A;Residues: 2020-2057 <PEE>
A;Cross-references: UNIPARC:UPI0000179213
A;Note: this peptide, designated proline-rich polypeptide V, can be found at several loc
A;Accession: A20593
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J. Biol. Chem. 258, 14206-14211.
A;Title: Proline-rich polypeptides bound to rat prostatic binding protein. The primary 8 A;Reference number: A94675; MUID:84061859; PMID:6685733
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                                                                                                                                                                                                                                          2033
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                                                                                                                                                1973
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|-----LIKDVPER---LYK--ELWDIVQT 1913
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                                                                                                                                1974 SSFSLLGVINTIQSRYLVDHSVENIRKLQLAKAQIQQLEAHMQENNVENLIQSLGAVRAV
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         GYAPQNISIRGEYQINFHIVNWNLSNPDPTSSEYITLIRDIQDKVTTLYKGSQLHD----
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                                                                                                                 ---TFRFCLVTNLTMDSV-
                                                     1882 G----RLCLEGDVRIPF-
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Molecule type: mRNA
Residues: 3372-3540 <HEM>
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A; Experimental source: strain S288C

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                                                                                                                                                                                                                         305 EPGPDE--PPTTPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFN 362
                                                                                                                                                                                                                                                                                                                                                                                                    363 STEGVLQHLLR-PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPG--- 418
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                                                                                                                                                                                                                                                                                                                          134 VLKNGGEDRLGVFDSFQK------STVAKMFP 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 VEEAIKLGVPKGPLFAKLTKG-----QTITL------DNGIVVTPEQVLENERH 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   494 DKV-TTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSN----LDPSLVEQVFLDKTL 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590 ------TITNLPYSQDKAQPGTTNYQRN-----KRNIEDALNQLFRNSSIKS 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 TGSALPSKYRNVVSTLVKVPFTD--ADGNTIN--RNIMLDAGENTLGTIHRMFSQLAVKS 528
                                                                                                       2.9%; Score 112.5; DB 2; Length 838;
19.1%; Pred. No. 14;
tive 82; Mismatches 173; Indels 203; Gaps
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C,Genetics:
MIPS:YKR079c
A;Gene: MIPS:YKR079c
A;Cross-references: SGD:S0001787
A;Map position: 11R
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Best Local Similarity 19.1*
Matches 108; Conservative
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.7
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US-10-952-535A-15
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APPLICANT: Boyle, Bryan
APPLICANT: Funk, Walter
APPLICANT: Funk, Walter
APPLICANT: Funk, Walter
APPLICANT: Funk, Walter
APPLICANT: Park, Eun Ju
APPLICANT: Park, Eun Ju
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
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APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: Tomizuka, Kazuma
APPLICANT: 2004-001-27
CURRENT APPLICATION NUMBER: US 60/519,241
PRIOR APPLICATION NUMBER: US 60/519,241
PRIOR PILING DATE: 2004-10-15
PRIOR PILING DATE: 2004-10-15
PRIOR PILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2004-03-03
PRIOR FILING DATE: 2008-08-30
NUMBER OF SEQ ID NOS: 182
SOCITURN OS: 182
SOCITURN OS
SOCITURN OS
SEQ ID NOS: 182
SEQ ID NOS: 182
SEQ ID NOS: 182
SEQ ID NOS: 182
SEQ ID NOS: 182
1675 WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYPNFTITNLPYSQDKAQPGTTHYQRNKR 1734
                                                                                             APPLICANT: Boyle, Bryan
APPLICANT: Boyle, Bryan
APPLICANT: Funk, Walter
APPLICANT: Kakitani, Makoto
APPLICANT: Oshima, Takeshi
APPLICANT: Park, Emily
APPLICANT: Tang, Y. Tom
APPLICANT: Tomizuka, Kazuma
APPLICANT: Yogi, Mikio
TITLE OF INVENTION: Gastrointestinal Proliferative Factor and uses thereof
FILE REFERENCE: 11926-1940.
CURRENT APPLICATION NUMBER: US/11/046,644
CURRENT FILING DATE: 2005-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                    614 NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
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                                                                                                                                                                                       1795 LEMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS 1831
                                                                                                                                                           674 LEMTRNGTOLONFTLDRSSVLVDGYSPNRNEPLTGNS 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 166.5; DB 7;
Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: GIPF V5His tag
                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/11046456
Publication No. US20050256044A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.2%;
Best Local Similarity 70.2%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-11-046-644-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               554 WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 SRKENITIERVLQGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP 133
                    Sequence 870, App
Sequence 868, App
                                                                                                                                                                                                                                                                                                    APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT PELLING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR PILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PATENTIN OF SEG ID NOS: 1452
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYBENNWPG
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Pred. No. 1.2e-287;
1; Mismatches 1;
                         US-10-995-561-870
US-10-995-561-868
                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                       Sequence 314, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.7%;
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Best Local Similarity 99.7
Matches 695; Conservative
                           1234
1366
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CRGANISM: Homo sapiens
US-11-033-039-314
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US-11-033-039-314
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SOFTWARE: Patentin Ver.
SEQ ID NO 16
LENGTH: 123
                    NUMBER OF SEQ ID NOS:
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Sequence 15, Application US/10952535A

Publication No. US2005255113A1

Sequence 15, Application US/10952535A

Publication No. US2005255113A1

APPLICANT: Huston, James S.

APPLICANT: Meser, Anne

APPLICANT: Lecerf, Jean-Michel

APPLICANT: Lecerf, Jean-Michel

TITLE OF INVENTION: MCCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS

TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS

TITLE OF INVENTION: MCCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS

CURRENT APPLICATION NUMBER: US/10/952,535A

CURRENT FILING DATE: 2004-09-27

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PATCHIN VET: 2.0
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APPLICANT: Leceff, Jean-Michel
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
FILE REPERENCE: INR-004CP
CURRENT APPLICATION NUMBER: US/10/952,535A
CURRENT FILING DATE: 2004-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: Construct US-10-952-535A-15
                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 PAKGNSADIQHSGGRSSLEGPRFEGKPIPNPLLGLDSTRTGHHHHHH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%; Score 134.5; DB 6; Length 98; 78.1%; Pred. No. 0.0005; tive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           705 PLTGNSADIQHSGGRSSLEGPRFEQKLISEEDLNM---HTGHHHHHH
                                                                                                                                                                                                                                                                                                                                                            Score 166.5; DB 7
Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             717 GGRSSLEGPRFEQKLISEEDLNMHTGHHHHHH 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 GGSTMSRGP-FEQKLISEEDLNWHTEHHHHHH 98
                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
PRIOR APPLICATION NUMBER. 2017
PRIOR FILING DATE: 2004-01-27
PRIOR PILICATION NUMBER: US 60/619,241
PRIOR PILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 178
SEQ ID NO 6
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/10952535A Publication No. US20050255113A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-07-27
                                                                                                                                                                                                                                                          ; FRATURE:
; OTHER INFORMATION: GIPF VSHis tag
US-11-046-644-6
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.2%;
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
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LENGTH: 98
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                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Construct
US-10-952-535A-16
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FORTHER INFORMATION: CONSTRUCT
OTHER INFORMATION: CONSTRUCT
OTHER INFORMATION: CONSTRUCT
OTHER INFORMATION: CONSTRUCT
OS-10-952-535A-17
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APPLICANT: Reddy, Ramachandra
APPLICANT: Reddy, Ramachandra
APPLICANT: Gill, Parkash
TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
TITLE OF INVENTION: ANGIGENESIS AND TUMOR GROWTH
FILE REPERRENCE: VASG-PO2-002
CURRENT APPLICATION NUMBER: US,10,949,720
CURRENT PILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US 60/454,432
PRIOR APPLICATION NUMBER: US 60/454,300
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                                                                                                                                                                 DB 6;
                                                                                                                                                               Score 134.5; DB 6
Pred. No. 0.00071;
1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Messer, Anne
APPLICANT: Lecerf, Jean-Michel
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WIT
FILE REPERENCE: INR-004CP
CURRENT APPLICATION NUMBER: US/10/952,535A
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/146,047
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
3.4%; Score 134.5; DB
Best Local Similarity 78.1%; Pred. No. 0.001;
Matches 25; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                         717 GGRSSLEGPRFEQKLISEEDLNMHTGHHHHHH 748
                                                                                                                                                                                                                                                                                                       717 GGRSSLEGPRFEOKLISEEDLNMHTGHHHHHH 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10952535A Publication Wo. US20050255113A1 GENERAL INFORMATION:
APPLICANT: Huston, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 419, Application US/10949720 Publication No. US20050249736A1 GENERAL INFORMATION: APPLICANT: Krasnoperov, Valery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zozulya, Sergey
Kertesz, Nathalie
Reddy, Ramachandra
Gill, Parkash
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                               Query Match
3.4%;
Best Local Similarity 78.1%;
Matches 25; Conservative
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ORGANISM: Artificial Sequence
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us-10-687-035-1.rapbn

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363 LTISDVSVLLIGGGERRYRAWVSAT---GISLGAMAGKGGGVSEWWLGIENGVLLLAGVV 419
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                                                                                                                                                                                                                                                                                                   303 SEMFLQIYKQGGFLGLSNIKFRPGSVVVQLTLAFREGTINVHDVETQFNQYKTEAASRYN 362
375 LFQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPYGPGLDIQQLYWELSQLTHG 434
                                                             --LTSSNHS 260
                                                                                                                                                               PRIOR PELICATION NUMBER: US 10/025,380
PRIOR APPLICATION NUMBER: US 09/922,217
PRIOR PILING DATE: 2001-12-19
PRIOR PELICATION NUMBER: US 09/922,217
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2001-04-10
PRIOR PILING DATE: 2000-08-28
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-19
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PRIOR PILING DATE: 2000-05-19
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-01-06
PRIOR PILING DATE: 2000-01-06
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
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PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 2000-01-16
PRIOR PILING DATE: 100-01-16
PRIOR PILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                 517 LIMDSVLVIV-----KALFSSNLDPSLVEQVFLDKTLNASFHWLG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557 ------STYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYS
                                                                                                                       135 VTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVN--WNLSNPDPTSSEYITLLRDI
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APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Fanger, Gary R.
APPLICANT: Variek Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILLS REFERENCE: 210121.471015
CURRENT APPLICATION NUMBER: US/11/108,172
                                                                                                                                                                                                                                                  493 QDKVTTLYK------GS---QLHDTFRFCLVT---
                                                 Sequence 1065, Application US/11108172
Sequence 1065, Application US/11108173
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.;
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 QDKAQPGTTNYQRNKRNIBDALNQL 622
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SSLEDPSTDYYQELQRDISEDVSDV 503
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
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APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Salceda, Susana
APPLICANT: Turner, Leah R.
APPLICANT: Turner, Leah R.
APPLICANT: Turner, Leah R.
APPLICANT: Liu, Yongming
APPLICANT: Dia, Compositions and Methods Relating to Breast Specific Genes and PT
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PT
TITLE REFERENCE: DEX-0432
CURRENT PLING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: US 60/389,327
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 171
SOFTWARE: Patentin version 3.1
SEQ ID NO 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 PAPGST-APPAHGVTSAPDNRPALGSTAPPVHNVTSASGSASGSASTIVHNGTSARATTT 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 PGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETRVDLLCTYLQPLS 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 169; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         632 FSDCQVSTFRSVP-----NRHHTGVDSLCNFSPLARR----VDRVALYEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 PEPVNVITIDREVPPAVSDIRVIRSSPSSLŠLAMAVPRAPSGAMLDYEVKYHEKGAEGPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
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                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 130; DB 6; Length 401
32.7%; Pred. No. 0.01;
tive 12; Mismatches 53; Indels
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19.5%; Pred. No. 0.037;
tive 63; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         719 RSSLEGPRFEQKLISEEDLNM---HTGHHHHHH 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 RSSLEGPRFEGKPIPNPLLGLDSTRTGHHHHH 401
                                                 PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/800,350
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 425
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 419
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 128, Application US/10517696; Publication No. US20060051759A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2%
Dest Local Similarity 19.5%
Matches 110; Conservative
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Best Local Similarity 32.74
Matches 50; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-949-720-419
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US-10-517-696-128
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APPLICATION NUMBER: US/11/193,561

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PRIOR FILING DATE: 2004-07-30
PRIOR PLING DATE: 2004-07-30
PRIOR PLING DATE: 2004-07-30
PRIOR PLING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 60/592,825
PRIOR PLLING DATE: 2004-07-30
PRIOR PLLING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 2
SEQ ID NO 2
                      CURRENT FILING DATE: 2005-07-29
PRIOR APPLICATION NUMBER: 60/592,823
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                                                                                                                                                                                                                                                                                                                                                   284 PARSTTSVILGESTTSPISSGSMETTALPG------STTTPGLS-----EKSTT 326
                                                                                                                                                                                                                                                          F----NTTERVLQGLLRPLFKNTSVGPLYSGCRLTLLRP----EKDGEATGVDAICTHR 127
                                                                                                                                                                                                                                                                                          62 TILLPDNITASGLLEASTPVHSST-----GSPHITLSPAGSTTROGESTTFQS-WPNS 113
                                                                                                                                                                                                                                                                                                                            PDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNG-----FTHRSSVPT---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                  224 HTISSAPSTTSALVEEPTSYHSSPGSTATTHFPDSSTTSGRSEESTASHSNQDATGTIVL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 ALRSVKN---GAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 F----HSSPRSPATTLSPASTTSSGVSEESTTSHSRPGSTHTTAFPDSTT--TPGLSRH 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SQESTISHSSPGST 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VGPGLDIQQLYWELSQLTHGVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIV 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SSP---GSTHTTLPPDSTTSSGIVEASTRVHS-----STGSPRTTLSP--A 481
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                                                                                                                                                                                       17 RSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYBENMWPGSRK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TINYORNKRNIEDALMOLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCNFSP 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEASTIPYSSPRSPITILSP----ASMISLGVGEESTISRSQPGSTHSTVSPASITIP 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YTGCRVI
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                                                                                                                                                       Gaps
                                                                                                                                                      Indels 280;
                                                                                                                    DB 7; Length 957; 0.29;
                                                                                                                                                                                                                                                                                                                                                                                               ----TSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNV--
                                                                                                                                                      81; Mismatches 269;
                                                                                                                                                                                                           20 QESTASHSSPGSTDTTLSPGSTTASSLGPESTTF---
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                                                                                                                    3.0%; Score 119; 19.0%; Pred. No. 0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1065
LENGTH: 957
                                                                                                                                    al Similarity 19.0
148; Conservative
                                                                   ; ORGANISM: Homo sapiens
US-11-108-172-1065
                                                                                                                    Query Match
Best Local S
Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595 SVEGSSTELNLPETANSV-----TLSDL-----QPG-VQYNITIYAVEENQES 636
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                                                                                                                                                                            297;
                                                                                                                 Length 2223;
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                                                                                                                 Query Match 3.0%; Score 118.5; DB 7; Best Local Similarity 18.9%; Pred. No. 1.2; Matches 171; Conservative 126; Mismatches 313;
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TYPE: PRT
ORGANISM: Homo Sapiens
                                                           US-11-193-561-2
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Sequence 2, Application US/11193561
Publication No. US20060024757A1
GENERAL INFORMATION:
APPLICANT: Husea, Robert
APPLICANT: Shorter, Simon
TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti

QY         314 TPKPATTFLPPLSEATTAMGYHLKTLTLINFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373           Db         757 DSTVLVRWTPPRAQITGYRL-TVGLTRRGQPRQYNVGPSVSKYPLR 801           QY         374 PLFQKSSMGPFYLGCQLISLRPBKDG-AATGVDTTCTYHPDPVGFGLDIQQLYWELSQLT 432	Db 802 NLQPASEYTVSLVAIKGNQESPKÄTGVFTTLQPGSSIPPYNTEVTETT 849  Qy 433 HGVTQLGFDR 445  :	QY 446 DSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQDKVTTLY 500	OY 501 KGSQLHDTPRRCLVTNLT	Qy 586 YLNFTITNLPYSQDKAQPGTTNYQRNKRNIEDALNQLFRNSSIKSYPSDCQV 637	OY 638 STFRSVENRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTRNGTQLQNFTLD 689	QY 690 RSSYLVDGYSPNRNEPLTGNSADIQHSGGRSSLEGFRFQKLISEEDLNNHT 741	Oy 742 GHHHHH 748  Db 1225 GYRIRHH 1231	RESULT 12 US-11-193-789-2 ; Sequence 2, Application US/11193789	; FULLICATION NO. 220000024,7234. ; GENERAL INFORMATION: ; APPLICANT: Hussa, Robert ; APPLICANT: Fisher-Colbrie, Mark	APPLICANT: Senyei, Andrew; APPLICANT: Senyei, Andrew; APPLICANT: Shorter, Simon; TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin	<b>422</b>	FRIOR FILING DATE: 2004-0/-30, 803  PRIOR PILING DATE: 2004-07-30  PRIOR PILING DATE: 2004-07-30  PRIOR PEPLICATION NUMBER: 60/592,825	APPLICATION N PILING DATE: APPLICATION N PILING DATE:	R OF SEQ ID NO ARE: FastSEQ : NO 2 TH: 2223 : PRT	, ORGANISM: Homo Sapiens US-11-193-789-2
Db 1070YTVTGLEPG-IDYDISVITLINGGESAPTTLTQQTAVPPFTDLRFTNIGP 1118  Qy 638 STPRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEFIRMTRNGTOLONFTLD 689	QY 690 RSSVLVDGYSPNRNEPLTGNSADIQHSGGRSSLEGPRFEQKLISEEDLANHT 741	:    1225 GYRIRHH	RESULT 11 US-11-193-771-2 ; Sequence 2, Application US/11193771 ; Fublication No. US20060024722A1 ; GENERAL INFORMATION: ; APPLICANT: Fisher-Colbie, Mark ; APPLICANT: Hiskok, Unilin ; APPLICANT: Hiskok, Unilin ; APPLICANT: Hiskok, Durlin ; APPLICANT: Hiskok, Durlin	; TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof; FILE REFERENCE: 17101-027001/828; CURRENT APPLICATION NUMBER: US/11/193,771; CURRENT FILING DATE: 2005-07-29	; PRIOR APPLICATION NUMBER: 60/592,823 ; PRIOR ELLING DATE: 2004-07-30 ; PRIOR APPLICATION NUMBER: 60/592,803 ; PRIOR FILING DATE: 2004-07-30	; PRIOR PEPLICATION NUMBER: 60/592,825 ; PRIOR FILING DATE: 2004-07-30 ; PRIOR APPLICATION NUMBER: 60/592,804 ; PRIOR FILING DATE: 2004-07-30		; INVETH: 2223 ; TYPE: PRT ; ORGANISM: Homo Sapiens US-11-193-771-2	Query Match 3.0%; Score 118.5; DB 7; Length 2223; Best Local Similarity 18.9%; Pred. No. 1.2; Matches 171; Conservative 126; Mismatches 313; Indels 297; Gaps 46;	QY 19 SVSTTSTPGTPTVYLGASKTPASIFGPSAASHLILEFTLMFTITNLRYE 67 : ::	Qy 68ENMMPGSRKENTTERVLQGLLRPLFKNTSVGPLYSGCRLT 107 ::     :	Qy 108 LLRPEKDGBATGVDAICTHRPDFTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLY 165  Db 554QTTAPDAPPDPTVDQVDDTSIVVRWSRPQAPITGYRIVYSP 594	QY 166 -VNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMQQPGSLKFNITDNVMKHL 221     : :     :     : :     : :     : :     : :       :   :         : :             : :	Qy 222 LSPLFQRSSLGARYTGCRVIALRSVKNGAETRVDLLCTYLQPL 264   :	697 HGQRLPISRNTFABVTGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKLDAPTNLQFVNET

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1119 DIMRVIWAPPPSIDLINFLVRYSPVKNEED---VAELSISPSDNAVVLINLLPGTEYVVS 1175
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                                                                                                                                                                                                                                                                                                                  -----ARYTGCRVIALRSVKNGAET--RVDLLCTYLQPL 264
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                                                                                                                                                SVEGSSTEINLPETANSV-----TLSDL-----QPG-VQYNITIYAVEENQES
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                                                                                            TTTSTSTPVTSNTVTGETTPFSPLVATSESVTEITASSFVVSWVSASDTVSGFRVEYELS
                                                                                                                           -------ENMWPGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLT
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                                                            19 SVSTTSTPGTPTVYLGAS-----KTPASIFGPSAASHLLILFTLNFTITNLRYE----
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Query Match
3.0%; Score 118.5; DB 7; Length 2223;
Best Local Similarity 18.9%; Pred. No. 1.2;
Matches 171; Conservative 126; Mismatches 313; Indels 297;
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RESULT 13 US-11-193-806-2 ; Sequence 2, Application US/11193806

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637 TPVVIQQETIGIPRSDIVPSPRDLQFVEVTDVKVTIMMIPPESÄVTGYRVDVIPVNLPGE 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 HGORLPISRNTFAEVTGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKLDAPTNLQFVNET 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 BEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDGEQSLILSTS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 SVSTTSTPGTPTVYLGAS-----KTPASIFGPSAASHLLILFTLNFTITNLRYE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 -VNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVM----KHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 SGPGLPI-KQVFHELSQQTHGIT---RLGPYSLDKDSLYLNGYNEPGPDEP-----PT
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                                                                                                                                                    Marker for Health
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.0%; Score 118.5; DB 7;
ilarity 18.9%; Pred. No. 1.2;
Conservative 126; Mismatches 313;
APPLICANT: Hussa, Robert
APPLICANT: Fisher-Colbrie, Mark
APPLICANT: Esher-Colbrie, Mark
APPLICANT: LaPointe, Jezome
APPLICANT: LaPointe, Jezome
APPLICANT: Shorter, Simon
TILLE OF INVENTION: Oncofetal Fibronectin as a Mi
FILE REFERENCE: 17101-028001/829
CURRENT APPLICATION NUMBER: 1065-07-29
FRIOR PILING DATE: 2004-07-30
FRIOR APPLICATION NUMBER: 60/592,823
FRIOR FILING DATE: 2004-07-30
FRIOR FILING DATE: 2004-07-30
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FRIOR APPLICATION NUMBER: 60/592,824
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US-11-193-806-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 171; Conserv
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Best Local S:
Matches 171
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222 LSPLFQRSSTELNLPETANSVTLSDLQDG-VQYNITIYAVEENQES 222 LSPLFQRSSLG	OY 638 STERSVUNRHHIGVDSLONFSPLARRVDRYALYEEFLANTRNGTQLONFILD 6899  1119 DTMRYTWAPPPSIDLTNFLVRYSPVRUBEDVABLSISPSDNAVVLTNLLFGTERVVS 1175  OY 690 RSSVLVDGYSPNRNEPLTGNSADIQHSGRSSLEGPRFEQKLISEEDLNNHT 741	US-11-133-561-17 ; Sequence 17. Application US/11193561 ; Publication No. US20060024757A1 ; GENERAL INFORMATION: ; APPLICANT: Husea. Robert ; APPLICANT: Shorter, Simon ; TITLE OF INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti; ; FILE REFERENCE: 17101-080001/831 ; FILE REFERENCE: 17101-080001/831 ; CURRENT APPLICATION NUMBER: 60/522,823 ; PRIOR APPLICATION NUMBER: 60/592,803 ; PRIOR PILING DATE: 2004-07-30 ; PRIOR PILING DATE: 2004-07-30 ; PRIOR PILING DATE: 2004-07-30 ; PRIOR FILING DATE: 2004-07-30 ; PRIOR PILING DATE: 2004-07-30 ; RIOR PILING DATE: 2004-07-30 ; RIOR PILING DATE: 2004-07-30
Db 961 NGQGGNSLEEVVHADQSSCTFDNLABGREXNVSVYTVKDDKESVPISDTIFEG 1014  Cy 533 NLDPSLVEOVFLDKT-LANSFHWLGSTYQLVDIHVTEMESSVYOPTSSSGTQHF 585  Db 1015PQLTDLSFYDITDSSIGLEWTPLANSS-TIIGYRITVVAAGEGIPFEDFVDSSVGY- 1069  Cy 586 YLMFTITULPYSQDKAQPGTTWYQRNKRNIEDALANQLFRNSIKSFFSDCQW 637  Db 1070YTVTGLEPG-INYDSSVTLINGGSSAPTLTNQCANAPPPTDLRFTWIGP 1118  Cy 638 STEKSVPRHHTGVDSLCAPSFLARRYDRAVITERELANTATORPPTDLRFTWIGP 1118  Cy 690 RSSVLVDGYSPRUREPLINFLARSVENEELANTATORPPTDLRFTWIGP 11175  Cy 690 RSSVLVDGYSPRUREPLARSVENEELARRYDRAVITELECTETVVS 1175  Cy 742 GHHHHH 748  Db 1176 VSSVYEQHESTPLRGRCKTGLDSFTGIDFSDITANSFTVHWIAPRATIT 1224  Cy 742 GHHHHH 748  Db 1125 GYRIRH 1231  RESULT 14  SEPULT 14  SPELICANT: HUSGN ROBET  APPLICANT: ESULT APPLICANTON NUMBER: 60/59-29  FRIOR APPLICANTON NUMBER: 60/59-29  FRIOR APPLICANTON NUMBER: 60/59-29	PRIOR FILING DATE: 2004-07-30 PRIOR FILING DATE: 2004-07-30 PRIOR APPLICATION NUMBER: 60/592,803 PRIOR PILING DATE: 2004-07-30 PRIOR PILING DATE: 2004-07-30 PRIOR PILING DATE: 2004-07-30 PRIOR PILING DATE: 2004-07-30 PRIOR PILING DATE: 2004-07-30 PRIOR PILING DATE: 2004-07-30 PRIOR FILING DATE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30 PRIOR PRIOR PARTE: 2004-07-30	ORGANISM: Homo Sapiens   3.0%; Score 118.5; DB 7; Length 2223;

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010 DSTVLVRWTPPRAQIT---GYRL-TVGLTRRGQPRQY------NVGPSVSKYPLR 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1103 IVITWIPAPRIGFKLGVRPSQGGEAPREVISDSGSIVVSGLIPGVEYVYTIQVLRDGQER 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1163 DAPIVNKVVTPLSPPTNLHLRANPDTGVLTVSWERSTTPDITGYRIT------TTPT 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 LLRPEKDGEATGVDAICTHRPDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLY-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 PLFQKSSMGPFYLGCQLISLRPEKDG-AATGVDTTCTYHPDFVGPGLDIQQLYWELSQLT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 DSLFINGYA-----PQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQDKVTTLY 500
                                                                                                                                                                                                                                                                                                                                                                                                -------ENMMPGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       848 SVEGSSTELNLPETANSV-----TLSDL-----QPG-VQYNITIYAVEENQES 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ARYTGCRVIALRSVKNGAET--RVDLLCTYLOPL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 KGSQ------LHDTFRFCLVTNLT-----------MDSVLVTVKALFSS 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 NLDPSLVEQVFLDKT-LNASFHW--LGSTYQLVDIHVTEMESS----VYQPTSSSSTQHF 585
                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVM---KHL 221
                                                                                                                                                                                                                                                                                                                                       :::||||| | :: | :| :: |: | | TITSTSTPVTSNTVTGETTPRSPLVATSESVTEITASSFVVSWVSASDTVSGFRVBYELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QTTAPDA----PPDPTVDQVDDTSIVVRWSRPQAPIT----GYRI-----VYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 HGVT-----OLGF------DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           638 STFRS--VPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTRNGTQLQN-----FTLD
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                  Indels 297;
                                                                                                                                                                                                                      DB 7; Length 2421
                                                                                                                                                                                                                                                                                                                                                                                                                                            758 EEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQISEDGEQSLILSTS
                                                                                                                                                                                                                    Query Match 3.0%; Score 118.5; DB 7; Best Local Similarity 18.9%; Pred. No. 1.3; Matches 171; Conservative 126; Mismatches 313;
                                                                                                                            ; DATABASE ACCESSION NUMBER: GenBank NM 212475
; DATABASE ENTRY DATE: 2005-06-10
US-11-193-561-17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPLFQRSSLG-----
                                                                                  ORGANISM: Homo Sapiens
PUBLICATION INFORMATION
                    SEQ ID NO 17
LENGTH: 2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1372
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Sequence 17, Application US/11193771

Sequence 17, Application US/11193771

Publication No. US20060024722A1

GENERAL INFORMATION:
APPLICANT: Fisher-Colbrie, Mark
APPLICANT: LaPointe, Jerome P.
TITLE OF INVENTION: Samples for Detection of Oncofetal Fibronectin and uses thereof
FILE REFERENCE: 17101-027001/828

CURRENT APPLICATION NUMBER: US/11/193,771

CURRENT FILING DATE: 2004-07-29

PRIOR FILING DATE: 2004-07-30

PRIOR PILING DATE: 2004-07-30

PRIOR PELING DATE: 2004-07-30

PRIOR PILING DATE: 2004-07-30

PRIOR PILING DATE: 2004-07-30

PRIOR PILING DATE: 2004-07-30

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PRIOR PILING DATE: 2004-07-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 -------BIMMPGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLT 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank NM 212475
DATABASE ENTRY DATE: 2005-06-10
                                                                                           1478 GYRIRHH 1484
742 GHHHHHH 748
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Publication No. US20060024724A1
GENERAL INFORMATION:
APPLICANT: HUSBA, Robert
APPLICANT: Fisher-Colbrie, Mark
                            SVSTTSTPGTPTVYLGAS
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----LOPGSSIPPYNTEVTETT 1102
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APPLICANT: Hussa, Robert
APPLICANT: Hussa, Robert
APPLICANT: LaPointe, Jerome
APPLICANT: LaPointe, Jerome
APPLICANT: Senyei, Andrew
APPLICANT: Shorter, Simon
TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
TITLE OF INVENTION: Methods for detecting Oncofetal Fibronectin
FILE REPERENCE: 17101-029001/830
CURRENT APPLICATION NUMBER: US/11/193,789
CURRENT FILING DATE: 2004-07-29
PRIOR PILING DATE: 2004-07-30
PRIOR PILING DATE: 2004-07-30
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   1055 NLQPASE----YTVSLVAIKGNQESPKATGVFTT---
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DATABASE ENTRY DATE: 2005-06-10
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                                                           --ENMWPGSRKFNTTERVLOGLLRPLFKNTSVGPLYSGCRLT 107
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698 TTTSTSTPVTSNTVTGETTPFSPLVATSESVTEITASSFVVSWVSASDTVSGFRVEYELS
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PRIOR APPLICATION NUMBER: 60/592,823
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Publication No. US20060024725A1
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GENERAL INFORMATION:
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19 SVSTTSTPGTPTVYLGAS-----KTPASIFGPSAASHLLILFTLNFTITNLRYE--
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DATABASE ACCESSION NUMBER: GenBank NM 212475
DATABASE ENTRY DATE: 2005-06-10
                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 60/592,804
PRIOR FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 60/,592,824
PRIOR FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                                                                            NR APPLICATION NUMBER: 60/592,823
NR FILING DATE: 2004-07-30
NR APPLICATION NUMBER: 60/592,803
NR FILING DATE: 2004-07-30
NR APPLICATION NUMBER: 60/592,825
NR FILING DATE: 2004-07-30
NR APPLICATION NUMBER: 60/592,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 17
LENGTH: 2421
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APPLICANT: Hussa, Robert
APPLICANT: Fisher-Colbrie, Mark
APPLICANT: Hickok, Durlin
APPLICANT: LaPointed, Jerome P.
TITLE OF INVENTION: Oncofetal Fibronectin as Marker for Pregnancy-Related Indications
                                                                       533 NLDPSLVEQVFLDKT-LNASFHW--LGSTYQLVDIHVTEMESS----VYQPTSSSSTQHF 585
                                                                                                                                                                                           586 YLNFTITNLPYSQDKAQPGTTNYQRNKRNI----EDALNQLFRNSSIKS----YFSDCQV 637
                                                                                                                    .268 ---PQLTDLSFVDITDSSIGLRWTPLNSS-TIIGYRITVVAAGEGIPIFEDFVDSSVGY- 1322
                                                                                                                                                                                                                                                                                 1323 ---YTVTGL-----EPG-IDYDISVITLINGGESAPTTLTQQTAVPPPTDLRFTNIGP 1371
1214 NGQQGNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPEV---- 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                1372 DIMRVIWAPPPSIDLINFLVRYSPVKNEED---VAELSISPSDNAVVLIVLLPGTEYVVS 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1429 VSSV----YEQHESTPLRG-----RQKTGLDSPTGIDFSD--ITANSFTVHWIAPRATIT 1477
                                                                                                                                                                                                                                                                                                                                                         638 STFRS--VPNRHHTGVDSLCNFSPLARRVDRVAIYEEFLRMTRNGTQLQN-----FTLD 689
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Matches 171; Conservative 126; Mismatches 313;
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DATABASE ENTRY DATE: 2005-06-10
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PRIOR PRILING DATE: 2004-07-30
PRIOR PILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FABLESC for Windows Version 4.0
SEQ ID NO 17
LENGTH: 2421
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18.9%; Pred. No. 1.3
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CURRENT APPLICATION NUMBER: US/11/193,857
CURRENT FILING DATE: 2005-07-29
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1103 IVITWTPAPRIGPKLGVRPSQGGEAPREVTSDSGSIVVSGLTPGVEYVYTIQVLRDGQER 1162
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                                                                                                                                                                                                                                                                                                   -------ENMWPGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGCRLT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVM---KHL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 NLDPSLVEQVFLDKT-LNASFHW--LGSTYQLVDIHVTEMESS----VYQPTSSSSTQHF
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                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                           Query Match 3.0%; Score 118.5; DB 7; Best Local Similarity 18.9%; Pred. No. 1.4; Matches 171; Conservative 126; Mismatches 313;
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ORGANISM: Homo Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank NM 212482
DATABASE ENTRY DATE: 2005-06-10
PRIOR FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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                                                                    LENGTH: 2477
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TITLE OP INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
TITLE OP INVENTION: Detection of Oncofetal Fibronectin for Selection of Concepti
CURRENT APPLICATION NUMBER: 08/11/193,561
CURRENT FILING DATE: 2004-07-29
FRIOR APPLICATION NUMBER: 60/592,823
FRIOR FILING DATE: 2004-07-30
FRIOR FILING DATE: 2004-07-30
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                                                                                                                                                                                                                                                                                   PLFQKSSMGPFYLGCQLISLRPEKDG-AATGVDTTCTYHPDPVGPGLDIQQLYWELSQLT 432
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                           --- ARYTGCRVIALRSVKNGAET---RVDLLCTYLQPL 264
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       -VNGFTHRSSVPTTSTGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVM---KHL
                                                                                                                                                                                                                314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
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                                                                                                                                             SGPGLPI-KQVFHELSQQTHGIT---RLGPYSLDKDSLYLNGYNEPGPDEP----PT
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Publication No. US20060024757A1
GENERAL INFORMATION:
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                             SVEGSSTELNLPETANSV
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                                                                          222 LSPLFQRSSLG
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APPLICANT: Soltis, Daniel A.
TILLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: CA 125/0712P AND METHODS OF USE THEREOF
FILE REFERENCE: 6750-214-999
CURRENT APPLICATION NUMBER: US/10/687,035
CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/418,986
PRIOR APPLICATION NUMBER: 60/418,986
PRIOR APPLICATION NUMBER: 60/418,986
PRIOR FILING DATE: 2003-10-12
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 748
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100.0%; Pred. No. 3.1e-312;
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ORGANISM: Artificial Sequence
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Matches 748; Conservative
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APPLICANT: Soltis, Daniel A.

APPLICANT: Soltis, Daniel A.

TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED

TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED

TITLE OF INVENTION: AL25/0772P AND METHODS OF USE THEREOF

FILE REFERENCE: 6750-214-999

CURRENT APPLICATION NUMBER: 05/10/687,035

CURRENT PILING DATE: 2003-10-15

PRIOR APPLICATION NUMBER: 60/486,986

PRIOR APPLICATION NUMBER: 60/418,828

PRIOR PELING DATE: 2003-10-12

NUMBER OF SEQ ID NOS: 71

SOFTWARE: FASTESEQ for Windows Version 4.0

IENGTH: 809
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US-10-687-035-2
                                                                                                                                                                                                                                748
                                                                                                                                                                                                                                                     721 SLEGPRFEQKLISEEDLNWHTGHHHHH 748
                                                                                                                                                                                                                                  SLEGPRFEOKLISEEDLNMHTGHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/10687035; Publication No. US20050064518A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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420 INNLRYMADMGQPGSLKFNITDNVMQHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR 6479
                                                                                                                                                5480 VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT 6539
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                                                                                                                                                                                                                             5540 TPKPATTPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 6599
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  3360 GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 6419
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                                                                                                                                                                                                       314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR 373
                                                                                                                                                                                                                                                                                    374 PLPOKSSMGPPYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 433
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                                                                                                                       254 VDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGPDEPPT
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                                          194 INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTG
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Patent No. US20020119158A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT APPLICATION NUMBER: 200106-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: PaetsEQ for Windows Version 3.0
SSEQ ID NOS 389
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Pred. No. 3.6e-289;
0; Mismatches 1;
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Best Local Similarity 99.9
Matches 696; Conservative
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; ORGANISM: Homo sapiens
US-09-884-441-389
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APPLICANT: Senter, Peter D.
APPLICANT: Senter, Peter D.
APPLICANT: Senter, Peter D.
APPLICANT: Senter, Peter D.
APPLICANT: Bens, Allen J.
APPLICANT: Bolakis, Paul
APPLICANT: Slawcowski, Mark X.
APPLICANT: Slawcowski, Mark X.
APPLICANT: Slawcowski, Mark X.
APPLICANT: Slawcowski, Mark X.
APPLICANT: Slawcowski, Mark X.
APPLICANT: Kline, Toni Beth
TITLE OF INVENTION: MONOMETHYLVALINE COMPOUNDS CAPABLE OF CONJUGATION TO LICANDS
FILE REPRENCE: 01891-001020US
CURRENT APPLICATION NUMBER: US 60/598,899
PRIOR PELING DATE: 2004-11-05
PRIOR PELING DATE: 2004-09-06
PRIOR APPLICATION NUMBER: US 60/557,116
PRIOR APPLICATION NUMBER: US 60/557,116
PRIOR APPLICATION NUMBER: US 60/518,534
PRIOR PILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 35
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                                                                                                            TSSEXITLLRDIQDKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVB
                                                                                                                                                                                  QVFLDKTLNASFHWLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDK
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Pred. No. 6.8e-288;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Doronina, Svetlana O. APPLICANT: Toki, Brian B. APPLICANT: Senter, Peter D.
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99.9%;
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Best Local Similarity 99.9
Matches 696; Conservative
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ORGANISM: Homo sapien
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                                                             618 WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
                                                                                                           GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT
                                                                                                                             GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEBPFTLNFT
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; FILE REPERRACE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827,271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE FastSEQ for Windows Version 3.0
SEQ ID NO 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 3663; DB 3;
Pred. No. 3.6e-289;
0; Mismatches 1;
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Best Local Similarity 99.93
Matches 696; Conservative
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ORGANISM: Homo sapiens
US-09-827-271-389
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       GLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
                                                          INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
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                                      INNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETR
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Publication No. US20030091580A1
GENERAL INFORMATION, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Render, Gaven P.
APPLICANT: Render, Gaven P.
APPLICANT: Render, Gaven P.
APPLICANT: Redd, Steven P.
APPLICANT: Redd, Steven S.
APPLICANT: Redd, Steven G.
APPLICANT: Carter, Darrick
APPLICANT: Octorer, Darrick
APPLICANT: Octorer, Darrick
APPLICANT: Albone, Earl
TITLE OF INVENTION: Compositions NUD METHODS FOR THE THEN
TITLE OF INVENTION: Compositions NUD DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 389
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99.9%; Pred. No. 3.6e-289;
live 0; Mismatches 1;
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ORGANISM: Homo sapiens
US-09-907-969-389
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                     STPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYBENMWPG 73
                                                                                               SRKFNTTERVLOGLLRPLFKNTSVGPLYSGCRLTLLRPEKDGEATGVDAICTHRPDPTGP
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; Publication No. US20050031634A1
; GENERAL INFORMATION.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Gary R.
; APPLICANT: RANGER, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833

"WADE: IRMST. INC.
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; PUblication No. US20030124140A1
; GENERAL INFORMATION.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Panger, Gary R.
; APPLICANT: Hill, Paul DIAGNOSIS OF OVARIAN CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT PILING BATE: 2002.07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: PastSEQ for Windows Version 4.0
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Pred. No. 3.6e-289;
0; Mismatches 1; Indels
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Best Local Similarity 99.5
Matches 696; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo
US-09-778-320-206
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                                       FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG
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                            FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG
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          Gaps
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Sequence 206, Application US/09778320

Sequence 206, Application US/09778320

Sequence 206, Application US/09778320

SERENTAL INPORMATION:

APPLICANT: Dilon, Davin C.

APPLICANT: Houghton, Raymond L.

APPLICANT: Mitcham, Jennifer

APPLICANT: Modell, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION UNDERS. US/09/778,320

CURRENT APPLICANT: WIGHER DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 301

SEQ ID NO 206

LENGTH: 914
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Pred. No. 3.6e-289;
0; Mismatches 1;
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  Similarity
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Patent No. US20020081609A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Diang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Houghton, Raymond L.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Marlocker, Susan L.
APPLICANT: Marlocker, Susan L.
APPLICANT: MARJONSTON: COMPOSITIONS
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.491C6
                                           Score 3663; DB 3;
Pred. No. 4.2e-289;
0; Mismatches 1;
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nilarity 99.9%;
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Best Local Similarity
Matches 696; Conserv
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Barent No. US20020119158A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION:
PILE REFERENCE: 210121.462C7
                                                                                                                                                                                                                Length 914;
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Pred. No. 4.2e-289;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/884,441,
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 312
LENGTH: 914
                                                                                                                                                                                                              Query Match
Best Local Similarity 99.9%;
Matches 696; Conservative
                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-441-312
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Pred. No. 4.2e-289;
0; Mismatches 1;
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APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
PILE REFERENCE: 210121.462C7
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CURRENT TILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: PARESEQ for Windows Version 4.0
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                                                                                                                                                                                                              Query Match
Best Local Similarity 99.9%;
Matches 696; Conservative
                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-689-206
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US-09-884-441-312
                                                                               SEQ ID NO 206
LENGTH: 914
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Pred. No. 4.2e-289;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 478
LENGTH: 914
                                                                                                           92.9%;
99.9%;
                                                                                                                                 696; Conservative
                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-478
                                                                                                            Query Match
Best Local Similarity
Matches 696; Conserv
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APPLICANT: Fanger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Albone, Earl
APPLICANT: Albone, Earl
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C8
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 312
LENGTH: 914
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92.9%; Score 3663; DB 3;
Best Local Similarity 99.9%; Pred. No. 4.2e-289;
Matches 696; Conservative 0; Mismatches 1;
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, ORGANISM: Homo sapiens
US-09-907-969-312
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RESULT

; Sequence 312, Application US/09907969; Publication No. US20030091580A1; GENERAL INFORMATION: APPLICANT: Mitcham, Jennifer L.; APPLICANT: King, Gordon E.; APPLICANT: Fling, Steven P.; APPLICANT: Fling, Steven P.; APPLICANT: Retter, Marc W.

RESULT 13 US-09-907-969-312

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614 NIEDALNOLFRNSSIKSYFSDCOVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF 673
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                                                                      710
                                                                                                                                                                                                                          Sequence 312, Application US/09827271

Publication No US20030165504A1

GENERAL INPORMATION:

APPLICANT: Retter, Marc W.

APPLICANT: Renger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

CURRENT APPLICATION UNDERER: 18/09/827,271

CURRENT FILING DATE: 2001-04-04

NUMBER OF SEQ ID NOS: 461

SEQ ID NO 312

LENGTH: 914
                                                                        674 LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS
                                                                                                   , ORGANISM: Homo sapien US-09-827-271-312
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US-09-827-271-312
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? OVARIAN CANCER
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TITLE OF INVENTION: COMPOSITIONS AND METHO
TITLE OF INVENTION: AND DIAGNOSIS OF OVAR
FILE REPERENCE: 210121.46208
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001.07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FRASESQ for Windows Version 4.0
                        Sequence 478, Application US/09907969 Publication No. US20030091580A1 GENERAL INFORMATION:
                                                                                    APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Fanger, Marc W.
APPLICANT: Renger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Hill, Paul
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Best Local Similarity 99.9
Matches 696; Conservative
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                                  614 NIEDALNQLFRNSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEEF
                                                                                                                                                                 74 SRKFNTTERVLQGLLRPLFXNTSVGPLYSGCRLTLLRPBKDGEATGVDAICTHRPDPTGP
               DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                              WLGSTYQLVDIHVTEMESSVYQPTSSSSTQHFYLNFTITNLPYSQDKAQPGTTNYQRNKR
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APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER;
FILE REPERENCE: 210121.462C9
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 312
LENGTH: 914
                                                                                                                                                                                                            674 LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS 710
                                                                                                                                                                                                                             Score 3663; DB 4;
Pred. No. 4.2e-289;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                           ; Sequence 312, Application US/10198053; Publication No. US20030124140A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-198-053-312
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APPLICANT: Jiang, Yuqiu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Moneill Patricia D.
APPLICANT: Wang, Tongtong
APPLICANT: Moneill Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Schentner, Barbara
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.491C7
CURRENT APPLICATION NUMBER: US/10/010,742
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FREESEQ for Windows Version 4.0
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                                                                  Query Match 92.9%; Score 3663; DB 4; Best Local Similarity 99.9%; Pred. No. 4.2e-289; Matches 696; Conservative 0; Mismatches 1;
                                                 LRMTRNGTQLQNFTLDRSSVLVDGYSPNRNEPLTGNS
                                                                                                                                                                ; Sequence 206, Application US/10010742; Publication No. US20020146727A1; GENERAL INFORMATION:
                                                                                                                                                                                                                 APPLICANT: Dillon, Davin C. APPLICANT: Day, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                   RESULT 16
US-10-010-742-206
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LENGTH: 914
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Publication No. US20040101899A1

GENERAL INRORMATION:

APPLICANT: Dillon, Davin C.

APPLICANT: Day, Craig H.

APPLICANT: Day, Craig H.

APPLICANT: Houghton, Raymond L.

APPLICANT: Micham, Jennifer B.

APPLICANT: Moneill, Particia D.

TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER

FILE REFERENCE: 210121.491D1

CURRENT PAPLICATION UNDEER: 2031-1-14

NUMBER OF SEQ ID NOS: 301

SEQ ID NO 206

LENGTH: 914
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Pred. No. 4.2e-289;
0; Mismatches 1;
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99.9%;
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Best Local Similarity 99.9
Matches 696; Conservative
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; ORGANISM: Homo sapien
US-10-714-389-206
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                                                                      NIEDALNQLFRNSSIKSYFSDCQVSTFRSVPNRHHTGVDSLCNFSPLARRVDRVAIYEFF
                                                     DKVTTLYKGSQLHDTFRFCLVTNLTMDSVLVTVKALFSSNLDPSLVEQVFLDKTLNASFH
                                                                                                                                        FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG
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Pred. No. 4.2e-289;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 478. Application US/10198053
Sequence 478. Application US/10198053
Sequence 478. Application No. US20030124140A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEFF
ITILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
ITILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
ITILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SSETWARE PRESENCE: Anidows Version 4.0
SSEQ ID NO 478
LENGTH: 914
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; ORGANISM: Homo sapiens
US-10-198-053-478
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TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLR
                 PLEQKSSMGPFYLGCQLISLRPEKDGAATGVDTTCTYHDDPVGPGLDIQQLYWELSQLTH
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Vargiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEIR
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
CURRENT APPLICATION NUMBER: 105/10/717,296
CURRENT FILING DATE: 2003-11-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 206
LENGTH: 914
                                                                                                                                                                                                  LEMTRNGTOLONFTLDRSSVLVDGYSPNRNEPLIGNS 710
                                                                                                                                                                                                              92.9%; Score 3663; DB 4;
99.9%; Pred. No. 4.2e-289;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                 ; Sequence 206, Application US/10717296
; Publication No. US20040142361A1
; GENERAL INFORMATION:
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Matches 696; Conservative
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ORGANISM: Homo sapiens
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US-10-717-296-206
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                                                                                                           GYTOLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEYITLLRDIQ
                    PLEOKSSMAPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVGFGLDIQQLYWELSQLTH
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Search completed: March 20, 2006, 07:35:08 Job time : 137.781 secs

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Q5bjz2 rattus norv
P01755 mus musculu
Q8vcx7 mus musculu
Q7tmt6 mus musculu
Q5fvp3 rattus norv
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q65ZL2_9MURI	Q65ZR6_MOUSE	QBK172 MOUSE	OSHZVE MOTISE	HV51 MOUSE	HV12 MOUSE	Q504M7 MOUSE	Q8K0F2_MOUSE		Q9QXE9 MOUSE	09240 MOUSE	092552 MOUSE	OSBK05 RAT	Q924R8_MOUSE	Q52L51_MOUSE	HV03 MOUSE	CAZUES MOUSE	Q924R0 MOUSE	QBVIJ1_MOUSE	Q924R4 MOUSE	Q924P8 MOUSE	HV09 MOUSE	Q91WT3 MOUSE	OSKSHO MOUSE	COSTANS MOUSE	HV04 MOUSE	Q924Q0 MOUSE	Q924P7_MOUSE	092401 MOUSE	HVU6 MOUSE	0924P5 MOUSE	Q505N9_MOUSE	HV50 MOUSE	Q924Q4 MOUSE	CASACA MOUSE HVOS MOUSE	HV49 MOUSE	Q924Q5 MOUSE	Q7TQM2_MOUSE	O924P9 MOUSE	Q9JL75 MOUSE	Q924R2_MOUSE	OCEOSS HUMAN	Q924Q8 MOUSE	Q6ZP87_HUMAN	Q7TPE3_MOUSE	COZAR/ MOUSE HVIO MOUSE	HV01 MOUSE	091V67 MOUSE	Q91VA2_MOUSE	092402 MOUSE	97176	924P6	6N030	Q8WY24 HUMAN O9.II.81 MOIISE	HUMA	HVIC HUMAN	4500m_tvc0cp
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                                                                                                                                                                                                                                               Expression driven by an MWTV-TER enhancer;

Expression driven by an MWTV-TER enhancer;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Rataubberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

Ratauberg R.L., Feingold E.A., Grouse C.H., Derged J.G.,

Ratauserg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raplecon M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W. Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley C.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSWIFLFLLSGTAGVHSEVOLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                       IISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
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Expression driven by an MMTV-LTR enhancer.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO18535; AAH18535.1; -; mRNA.
HSSP; P01865; 1KB5.
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                                                                  Last sequence update)
Last annotation update)
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Best Local Similarity 79.6%; Pred. No. 1.4e-48;
Matches 117; Conservative 6; Mismatches 11
                          472 AA.
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GO; GO:0003823; F:antigen binding; IEA
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                          PRT;
                                                      Created)
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InterPro; IPR007110; Ig-like.
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
'fam; PP07654
                                                    05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF07654; C1-set; 3.
                       QEPJA7 MOUSE PRELIMINARY;
Q6PJA7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
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                                                                                             Hypothetical protein.
Name=Igh-la;
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                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                 NCBI_TaxID=10090;
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              MOUSE
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ALAMEN'ESUBSECTO, PubMed=1247932; DOI=10.1073/pnas.242603899;
A REDLINE=22388257; PubMed=1247, Grouse L.H., Derge J.G.,
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Rlauener R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
A lischul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,
A lischul S.F., Dordan H., Moore T., Max S.I., Wang J., Heieh F.,
A popkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A papleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A propertion M.J., Uschin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pathey J., Helton B.K. Ketreman M., Madan A., Xoung A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
Brinerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Brinerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                    61 GKSLEWIGYIYPNNGGNGYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAR--- 117
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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Hypothetical protein.
SEQUENCE 483 AA; 52436 MW; 368B7BEEGB6DE9EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
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80.6%; Pred. No. 4.2e-48;
iive 9; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                             483 AA
                                                                                                                                   139
                                                                                                                                                                                        118 --GYISYYSYDHYFDYWGQGTTITVSS 142
                                                                                                                                   121 GSGY-----YFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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STRAIN=FVB/N; TISSUE=Colon;
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Best Local Similarity 80.6'
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                             Q4VAB6 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FVB/N;
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121 -GSGYYFDYWGQGTTLTVSS 139
                 121 SGSYWYFDVWGAGTTVTVSS
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                                                                                                                                                                                                                                                              Expression driven by an MATV-LTR enhancer;

X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,

A Richards S., Worley K.C., Hale S., Garcial A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Budfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSWIFLFLESGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSWVPLFLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTPTGYYMHWVKQSH
                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Mammary tumor metastatized to lung. MMTV-LTR/Whtl model. Expression driven by an MMTV-LTR enhancer.; Strausberg R.; Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BCO55910; AAH55910.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                     IISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.2%; Score 585.5; DB 2; Length 90.0%; Pred. No. 4.5e-47; ive 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n; Immunoglobulin domain.
51728 MW; 6D90E4DF896BB090 CRC64;
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PP07654; C1-8et; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMATT; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                  01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein AI324046.
                                        Q7TMK1;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
            Q7TWK1 MOUSE DRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 80.0
hes 112; Conservative
                                                                                                                                                                              Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein;
SEQUENCE 470 AA; 51
                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEOUENCE,
                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CZECH II;
                                                                                                                                                                                                                                         STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                                                                                                                   Name=AI324046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                             Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.; "Diversity of germ-line immunoglobulin VH genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.4%; Score 579; DB 1; Length 117; Best Local Similarity 92.3%; Pred. No. 3.9e-47; Matches 108; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region 108A
Ig-like.
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                 10-MAY-2005 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g heavy chain V region 108A precursor.
Name-1gh-VJ558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 AA
     117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J00488; AAA38519.1; -; Genomic_DNA.
PIR; A02041; HVMS8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81245215; PubMed=6789211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01751; INQB.
SMR; P01758; 20-116.
MGI; MGI: 96446; Igh-U3558.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSS0835; IG LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q58E56_MOUSB PRELIMINARY;
Q58E56;
                                                                                                                                                                                                                                                                                                                                                                                                             "Diversity of germ-line ir
Nature 292:426-430(1981).
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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HV14 MOUSE
P01758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSGBBHHRB
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                                                                                                                                                           Expression driven by an NMTV-LTR enhancer;

Expression driven by an NMTV-LTR enhancer;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Margner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsheh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Repleton M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robert S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

Richards S.A., McEwan P.J., McKernan K.J., Nalek J.A., Guibs R.A.,

A Richards S.A., Wolley K.C., Hale S., Garcia A.M., Gabb R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Reneration and initial analysis of more Honls. 15,000 full-length human mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MG1; MG1:9643; 1gh-1a.

MG1; MG1:9643; 1gh-1a.

G0; G0:0005731; C:immurgolobulin complex, circulating; IDA.

G0; G0:0005731; C:multivesicular body. IDA.

G0; G0:0001788; P:antigen binding; IDA.

G0; G0:0001788; P:antigen processing; IDA.

G0; G0:000533; P:antigen processing; IDA.

G0; G0:000533; P:antigen processing; IDA.

G0; G0:000533; P:antigen processing; IDA.

G0; G0:000531; P:antigen processing; IDA.

G0; G0:000531; P:antigen processing; IDA.

G0; G0:000531; P:antigen processing; IDA.

G0; G0:000531; P:phagocytosis, recognition; IDA.

G0; G0:005077; P:positive regulation of immune response; IDA.

G0; G0:0050778; P:positive regulation of immune response; IDA.

G0; G0:0001912; P:positive regulation of thype IIA hypersensitivity; IDA.

G0; G0:0001912; P:positive regulation of type IIA hypersensitivity; IDA.

G0; G0:0001912; P:regulation of type IIA hypersensitivity; IDA.

G0; G0:0001928; P:regulation of type IIA hypersensitivity; IDA.

G0; G0:0001928; P:regulation of type IIA hypersensitivity; IDA.

G0; G0:0001928; P:regulation of proteolysis and peptidolysis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; IDA.
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
                                                                                                                                                 FISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.9%; Score 575.5; DB 2; Length 477; Best Local Similarity 77.5%; Pred. No. 4.1e-46; Matches 110; Conservative 10; Mismatches 19; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC092061; AAH92061.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMUGGUS; LC. LIKE; 4.
PROSITE; PS50839; IG_MHC; UNKNOWN 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
477 AA: 52222 MW; S19211BE5EA12364 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression driven by an MMTV-LTR enhancer.; NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO, GO:U0JULE.
InterPro; IPR001599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                      LEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CZECH II;
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TISSUE-Mammary tumor. WAP-TGF alpha model. 7 months old;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RIAUSNER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RADA S.F., Jordan H., Moore T., Max S.I., Mang J., Heiseh F.,

A Depkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiseh F.,

Raba S.A., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Malek J.A., Gubs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rada S.C., Grimwood J., Schmutz J., Myers R.M.,

Rodisquez A.C., Grimwood J., Schmutz J., Whers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Teleneration and initial analysis of more than 15,000 full-length human
                                                                 61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWD- 119
1 MGWSWIFLFLLSGTAGVLSEVQLHQSGPELVEAGASVKLSCKASGYTFGDYYVHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52326 MW; 52B44C5826807143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                      481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl. ENSWUGGG0000021155; Mus musculus. GO; GO:0003823; F:antigen binding; IEA. InterPro; IPR007110; Ig_like. InterPro; IPR003597; Ig_cl. InterPro; IPR003597; Ig_cl. InterPro; IPR003066; Ig MHC. Fro: IPR003066; Ig WHC. Fro: IPR003566; Ig V. Fro: IPR00556; Ig V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC018455; AAH18455.1; -; mRNA.
HSSP; P01810; 2FBJ.
SMR; Q8VCV5; 20-239.
                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                          120 --FGSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences."
                                                                                                                                                                                                                                                                    QBVCVS_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mmunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 AA;
                                                                                                                                                                                                                                                                                                                                                                        LOC238447 protein.
Name=LOC238447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH MGC Project
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Query Match

52965 MW; F12068460B400B9D CRC64;

488 AA;

SEQUENCE

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Anther Poly (1922) Anther Principle (1972) Anther Principle (1972) Anther Principle (1972) Anther Principle (1972) Anther Principle (1972) Anther Principle (1972) Anther Principle (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Antender (1972) Ant
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                                                                                                                                                                                                                                                                                                                              61 GKSLEWIGYIDPYNGGSSYNGKFKGKATLITVDKSSNTAFMYLNNLTSEDSAFYYCAREWY 120
                                                                                                                                                               1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                                  Gaps
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Submitted (SRP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SRP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013539; AAH13539.1; -; mRNA.
HSSP; P01751; 1A6W.
Ensembl; ENSWUSG0000021155; Mus musculus.
MG1; MG1:96486; 1gh-VG5S9.
InterPro; 1PR00110; 1g-1ike.
InterPro; 1PR001597; 1g c1.
InterPro; 1PR003596; 1g wHC.
InterPro; 1PR003596; 1g wHC.
InterPro; 1PR003596; 1g v.
Pfam; PF07654; C1-set; Z.
                                              19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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    Pred. No. 5.1e-45;
                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: :| :|||| :||||
121 GA--WFAFWGQGTLVTVSA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GSGYYFDYWGQGTTLTVSS 139
75.5%;
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STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=FVB/N; TISSUE=Kidney;
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Best Local Similarity 75.59
Matches 105; Conservative
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Name=Igh-VJ558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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MEDLINE-2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
X Strausberg R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
X Alacchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Alacchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
A Raba S.S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,
Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Generch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                  61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                  1 MGWSWIPLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                               Gaps
                                                                                                                                                                                                        10;
    Length 488;
Query Match 73.2%; Score 555; DB 2; Length 48: Best Local Similarity 72.6%; Pred. No. 3.7e-44; Matches 106; Conservative 13; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Ensembl; ENSWIGSGORO0021155; Mus musculus.
GO; GO:0003821; F:antigen binding; IEA.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_WHC.
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                                                                                                                                                                                                                                                                                                         EMBL; BC013490; AAH13490.1; -; mRNA.
HSSP; P01751; 1A6W.
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SMART; SMOAD6; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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Mus musculus (Mouse)
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RC TISSUE-Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

Expression driven by an MMTV-LTR enhancer;

RA MIDINE=238827; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

RA Alteschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

RA Alteschul S.F., Solates M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malak J.A., Gunarathe P.H.,

RAchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Nollalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RACHARD M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,

RA Nollalon D.K., Muzny D.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y. S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RACH M. Manna and initial analysis of more than 15,000 full-length human
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Czech II;
TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BUBL; BC018280; AMH18280.1; -; mRNA.
RHSSP; P01865; LTS.
RMI; Q6PJB2; 20-461.
RMI; MG1:96443; Igh-1a.
RMI; MG1:96443; Igh-1a.
RG0; G0:000382; F:antigen binding; IEA.
InterPro; IPR00319; Ig.
InterPro; IPR00310; Ig-1ike.
RINTERPO; IPR003309; Ig.
RINTERPO; IPR003306; Ig-MHC.
RINTERPO; IRR03306; Ig-MHC.
RINTERPO; IRR03306; Ig-MHC.
RINTERPO; IRR03306; Ig-MHC.
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SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                  465 AA
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                                                                                                 120 FGSGYYFDYWGQGTTLTVSS 139
                                                                                                                                    27,
27,
27,
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QEPJB2;
05-JUL-2004 (TrEMBLrel. 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Czech II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Igh-la;
                                                                                                                                                                                                                                                                               Q6PJB2 MOUSE
                                                                                                                                                                                                                                                                                                                        DDD BERTH DER RECCO ON SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SERVER RECEDENCE OF SER
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                                                                                                                                                                                                                                                                                                                                                                                 61 GKILLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWD- 119
                                                                                                                                                                                                                                                                                                                                                  GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                          1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                  1 MGWRWIFLFRLLSGTAGVQCQVQLLQSGPELVKPGASVKISCKASGYTFTSYYIHWVKQRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. NCBI TaxID=10090;
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InterPro; IPR003596; Ig_v.
SMART; SM00406; Ig_v.
IGV; 1.
PROSITE; PS50835; IG_IKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin heavy chain.";
Science 216:309-311(1982).
-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21152818; PubMed-6801765; Sime J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W., Capra J.D.;
                                                                                                     DB 2; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Somatic mutation in genes for the variable portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.3%; Score 532.5; DB 1; Length 1
74.3%; Pred. No. 1.3e-42;
ive 12; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region 93G7 Ig-like.
                                                                                                                                                                 Indels
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            Immunoglobulin domain.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
                                                                                                 70.4%; Score 533.5; DB 2; 74.1%; Pred. No. 4e-42; iive 9; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-WAY-2005 (Rel. 47, Last annotation update)
19 heavy chain V region 93G7 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AA
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HSSP; P01747; 1JFQ.
SMR; P01746; 20-140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSGYYFDYWGOGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGWAFDYWGQGTTLTVSS 136
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                                                                                                                              Best Local Similarity 74.1
Matches 103; Conservative
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P01746;
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SEQUENCE
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Best Local S
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                                                                                                     Query Match
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MEDLINE-22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Felmgold R.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jecherg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Joanes M.B., Bonaldo M.F., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A. Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,
A. Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                     61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                 1 MGWGWVFLFLLSVTAGVHTQVQLKQSGAELVKPGASVKLSCKASGYTFNSYIMHWVKQRP 60
                                                                               1 MGWSWIPLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !ISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                 .
9
              Length 465;
                                               21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .nd mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
            ;; Score 531; DB 2;
;; Pred. No. 6.7e-42;
11; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                          PRT;
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EMBL, BC092271; AAH92271.1; -; mRNA.
SMR; Q569W9; 20-464.
MGI; MGI:96443; Igh-1a.
GO; GO:0003823; F:antigen binding: I
                                                                                                                                                                                                                                      --GYYVFDYWGQGTTITVSS 135
                                                                                                                                                                                                                     121 GSGYY-FDYWGQGTTLTVSS 139
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              70.1%;
ilarity 72.9%;
Conservative 1
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InterPro; IPR003006; Ig_MHC
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10-MAY-2005 (TrEMBLrel
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                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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            Query Match
Best Local Similarity
Matches 102; Conserv
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RBHL outeration the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way, modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GQGLEWIGHIYPGNGYTEYNEKFKGKATLTSDTSSSTAYMQLRSLTSENSAIYFCAR--- 117
                                                                                                                                                                                                                                                                                                                                                             1 MEWSCIFLFLLSVTAGVHSEVQLQQSGAELVRPGSSVKLSCKTSGYTFTSYYINWVKQRP 60
                                                                                                                                                                                                                                                                                                                          1 MGWSWIFLFRLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Heary chain, variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus
                                                                                                                                                                                                                                                                Gaps
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MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIKB; 1.
jlobulin domain; Immunoglobulin V region; Signal
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                                                                                                                                                                                                                                                                s,
                                                                                                                                                                                                   Length 468;
                                                                                                                                                                                                                                                                Indels
                                                                                                      Hypothetical protein.
SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;
                                                                                                                                                                                                69.3%; Score 525.5; DB 2
72.3%; Pred. No. 2.3e-41;
iive 15; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1996 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g heavy chain V region B1-8/186-2 precursor
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InterPro; IPR007110; Ig-like.
SMAKI; SMOU40!; 16C1; 3.
SMAKI; SMOU406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GSGY--YPDYWGQGTTLTVSS 139
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PDB; 1NGQ; X-ray; H=20-139.
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                                                                                                                                                                                          Query Match
Best Local Similarity 72.3
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGv; 1
PROSITE; PS50835; IG I
3D-structure; Immunogl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01751; P01752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
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This Swiss-Prot entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                           "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes.";

From Jaccht CA genes.";

Proc. Natl. Acad. Sci. US.A. 79:2996-3000(1982).

-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVIS MOUSE STANDARD; PRT; 136 AA.
P01759;
21-JUL-1986 (Rel. 01, Leated)
21-JUL-1986 (Rel. 01, Leat sequence update)
10-MAY-2005 (Rel. 47, Leat annotation update)
10 heavy chain V region BCL1 precursor.
Nus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE-82222262; PubMed-6806821;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner P.R.;
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                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1.
                             Complementarity-determining-2
                                                                                                                                                                                                                                                                                                              15419 MW; 1B57DD4FD0C9F465 CRC64;
                                                                       By similarity
Framework-1.
                     Framework-2.
                                          Framework-3.
                                                           segment
                                                  D segment.
JH2 segment
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                                                                                                                                                                                                                                                                                                                                                         Matches 100; Conservative
                                                                                                                                                                                                                                                           109
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139 AA;
                                                                                                                                                                                                                                                                                                                                               Similarity
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NON TER
STRAND
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Murcidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region BCL1.
Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 67.9%; Score 514.5; DB 1; Local Similarity 70.5%; Pred. No. 6.2e-41; hes 98; Conservative 11; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 AA
                                                                                                                                                                                                                                                                                                                     PIR; A02042; HVWSB1.
HSSP; PO1751; INQB.
SMR; PO1759; 20-136.
Ensembl; ENSW1SG0000063048; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SW00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                         EMBL; J00494; AAA38130.1; -; Genomic_DNA
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ID Q58E61 MOUSE PRELIMINARY;
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135
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NUCLEOTIDE SEQUENCE.
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GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                            IISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer.;
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Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.5%; Score 512; DB 2; Length 485; 71.5%; Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Indels
                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. EMBL; BC092056; AAH92056.1; -; mRNA. GO:0003823; F:antigen binding; IEA.
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Last annotation update)
                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GSGYY-----FDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 --TYYSYDGGFAYWGRGTLVTVSA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-c1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4V9V8 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro, IPR003599; Ig
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                                                                                                                                                                                                                              STRAIN=Czech II;
                                                                                                                                                                                                                                                                                                                                NIH MGC Project,
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61 GGGLEWIARIYPGSGNTYYNEKFKGKATLTAEKSSTAYMQLSSLTSEDSAVYFCAR--- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSWIPFFLLSGTAGVHCQVQLKQSGAELVRPGASVKLSCKASGYTFTDYYINWVKQRP 60
      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heieh F.,
Diatchenko L., Marusina K., Fermer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor. WAP-TGF alpha model. 7 months old,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64892 MW; D425318F9A188B14 CRC64;
                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.5%; Score 512; DB 2;
70.5%; Pred. No. 5.6e-40;
iive 16; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG LIKE; 5.
PROSITE; PS00290; IG WHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                        BC096667; AAH96667.1; -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 -TGTGMDYWGQGTSVTVSS 135
                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR003597; Ig_cl.
nterPro; IPR003006; Ig_MHC
nterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70....
Best Societative
The State of Conservative
                                                                                                                      cDNA sequences.
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                                                                                                                                                                                                                                                  Submitted (MAY-2005) to
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01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                         TISSUE=Mammary gland;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 590 AA; (
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                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
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Name=LOC238447:
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                                                                                                                                                                                                                                Project
                                                                                                                                                                                                                                                                                          MGI; MGI:96448;
                                                                                                                      and mouse
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61 GKILJEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGWRWIFLFLLSGTAGVHCQVQLQQSGPELVKPGALVXISCKASGYTFTSFDISWWKQRP 60
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.B., Schnutz J., Myers R.M., Schein J.B., Sohnerch A., Schein J.B., Sonnes S.J.M., Marza M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 day old male pancreas CDNA, RIKEN full-length enriched library, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin domain.
SEQUENCE 480 AA; 51646 MW; 8690A63C669CDBED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Ensembl; ENSWIGSGORO00221155; Mus musculus.
GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig V.
Pfam; PF07654; Cl-set; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC029188; AAH29188.1; -; mRNA.
HSSP; P01820; 1G7J.
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70.5%;
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Q9D8L4;
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                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.
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Q9D8L4 MOU
Q9D8L4 MOU
Q9D8L6
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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M. Hanagaki T., Rara A., Itoh M., Izawa M., Kasukawa T., Kato H.,
M. Kawai J., Kojima Y., Konon H., Kouda M., Koya S., Kurihara C.,
M. Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
M. Asaaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sano H., Saaki D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T.,
M. Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
Muramateu M., Hayashizaki Y.;
Muramateu M., Hayashizaki Y.;
Submitted (JUL-2000) to the BMBL/GenBank/DDBJ databases.

EMBL; AK007918; BAB25349.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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                                                                                                                                                         STRAIN=C57BL/6J; TISSUB=Pancreas;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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The FANTOM Consortium,
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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              Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C., Braha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McErnan K.J., Malek J.A., Gunaratne P.H., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman M.W., Green B.D., Dickson M.C., Sutterfield Y.S. M., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; Schill human and initial analysis of more than 15,000 full-length human and mouse CDNA seciences.
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC Project;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
EMBL; BC091272; AAH91272.1; -; mRNA.
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PROSITE; PSSOB5; IG LIKE; 4.
Immunoglobulin domain; Repeat.
SEQUENCE 458 AA; 50161 MW; AOA61DCDD2CA433E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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66.2%; Score 501.5; DB 2.

Best Local Similarity 69.8%; Pred. No. 4.2e-39;

Matches 97; Conservative 14; Mismatches 25.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
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INCERPO, IPR003599; IG.
INCERPO, IPR007110; IG-like.
INCERPO, IPR003597; IG.
INCERPO, IPR003597; IG.
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                                                              NRI, 090844; 20-469.

SNRI, 090844; 20-469.

REASEMBLY: ENSWIGSGO0000054328; Mus musculus.

REASEMBLY: ENSWIGSGO0000054328; Mus musculus.

RG1, 6G1.96443; 1gh-1a.

RG2, GG:00042571; C:imminglobulin complex, circulating; IDA.

GG; GG:0003823; F:antigor binding; IDA.

GG; GG:0001788; P:antigor processing; IDA.

GG; GG:0001788; P:antigor processing; IDA.

GG; GG:0006528; P:complement activation, classical pathway; IDA.

GG; GG:0006533; P:early endosome to late endosome transport; IDA.

GG; GG:0006313; P:phagocytosis, engulfment; IDA.

GG; GG:0006910; P:phagocytosis, engulfment; IDA.

RG; GG:0050718; P:positive regulation of immune response; IDA.

GG; GG:0005078; P:positive regulation of phagocytosis; IDA.

GG; GG:0001788; P:positive regulation of type IIDA.

RG5; GG:0001788; P:positive regulation of type IIDA.

RG5; GG:0001788; P:positive regulation of type IIDA.

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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.L., Peingold B.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
66.3%; Score 502.5; DB 2; Length 473;
Best Local Similarity 70.4%; Pred. No. 3.5e-39;
Matches 100; Conservative 14; Mismatches 21; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Last annotation update)
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG_C1.
InterPro; IPR0035697; Ig_MHC.
InterPro; IPR003569; Ig_MHC.
InterPro; IPR003569; Ig_V.
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QSBJZ2;
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SEQUENCE 473 AA; 5
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                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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"Heavy chain variable region contribution to the NPb family of antibodies: sometic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: The gamma-2a chain mRNA was cloned from a hybridoma making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity-determining-1.
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Last annotation update)
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D segment.
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Framework-1
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SMR; P01755; 20-137.
InterPro; IPR007110; Ig-like.
InterPro; IPR003595; Ig_V.
SMART; SM0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
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Q8VCX7;
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                                                                                                                                                                                                                 (NPB antibodies).
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Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Browstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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T. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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BMBL; BCQ18315; AAH18315.1; -; mRNA.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
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PROSITE; PS00290; IG MHC; UNKNOWN_3.
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STRAIN=FVB/N; TISSUE=Salivary gland;
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Best Local Similarity
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Mon Mar 20 08:49:46 2006

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117 RWDFGSGYYFDYWGOGTTLTVSS 139

Search completed: March 20, 2006, 07:32:04 Job time: 26.0454 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

March 20, 2006, 07:29:34; Search time 5.07199 Seconds (without alignments) 2636.859 Million cell updates/sec Run on:

US-10-687-035-34
758
1 MGWSWIFLFLLSGTAGVHSE......FGSGYYFDYWGQGTTLITVSS 139 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database :

PIR\_80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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A;Cross-references: UNIPARC:UPI0000176D36
A;Experimental source: cell line 4C11
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchol C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchol C;Comment: This protein is an anti-idiotypic antibody in memoglobulin Newion; immunoglobulin memoglobulin memoglobulin sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status predicted <SIG>F;2-11/Domain: immunoglobulin homology <IMM:
F;34-117/Domain: immunoglobulin homology <IMM:
F;69-85/Region: complementarity-determining 1
F;118-125/Region: complementarity-determining 3
F;118-125/Region: Complementarity-determining 3
F;118-125/Romain: C region (fragment) #status predicted <COR>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLISEDSAVYYCAR 117
                                                                                                                                                                              Ign heavy chain precursor V region (108A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
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R,Givol, D.; Zakut, R.; Effron, K.; Rechavi, G.; Ram, D.; Cohen, J.B.
Nature 292, 426-430, 1991
A;File: Diversity of germ-line immunoglobulin V-H genes.
A;Reference number: A02041; MUD: 81245215; PMID: 6789211
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R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H. Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0011
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A;Accession: A02041
A;Molecule type: DNA
A;Residues: 1-117 (421V>
A;Cross-references: UNIPROT:P01758; UNIPARC:UPI00000270F3
A;Note: the sequence was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 1.9e-41;
9; Mismatches 18;
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Query Match
Best Local Similarity 78.4%;
Matches 109; Conservative
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8; Conservative
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A;Residues: 1-151 <CHE>
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                                                                                                                                           Ig heavy chain precursor V region (129) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999 C; Accession: A27609 #s. Sirlin, S.; Stavnezer, J.
B; Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A; Title: I.29 Jymphoma cells express a nonmutated V-H gene before and after H chain swith A; Reference number: A27609; MUID:88154467; PMID:3126234
A; Accession: A27609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP10000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PI
C;Genetics:
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Ig heavy chain precursor V region (BXW16) - mouse
C;Species Mus musculus (house mouse)
C;Species Hus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler: R.; Strobal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J.Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
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C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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80.6%; Pred. No. 4.4e-43;
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9; Mismatches
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80.6%; Pred. No. 4.3e
ive 10; Mismatches
         ALIGNMENTS
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Matches 112; Conservative
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Matches 112, Conservative
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R; Giusti, A.M.; Manser,
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                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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C;Keywords: immunoglobulin
GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
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A;Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:g262657
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 565.5; DB 2; Length:
Pred. No. 2.1e-41;
8; Mismatches 17; Indels
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A;Reference number: S37483
A;Accession: S37483
A;Setus: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                heavy chain (myeloma M104E) - mouse (fragment)
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                                                        GSGYYPDYWGQGTTLTVSS 139
                                                                             :||| || || || -- DWYFDVWGAGTTTVTVSS 136
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Best Local Similarity 79.9%;
Matches 111; Conservative
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R; Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G. Mol. Immunol. 27, 901-909, 1990
A; Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain A; Reference number: PHO105; MUID:91015092; PMID:2120577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reaidues: 1-138 <NEA>
A;Reaidues: 1-138 <NEA>
A;Cross-references: UNIPARC:UPI0000115EC4; GB:X56622; GB:S44836; NID:g49875; PIDN:CAA399:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                      anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                 Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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;;Species: Whus musculus (house mouse)
;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
;Accession: PH1482; PH1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.4%; Score 548.5; DB 2; Best Local Similarity 74.8%; Pred. No. 5.8e-40; Matches 104; Conservative 16; Mismatches 18;
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A; Experimental source: hybridoma cell
                                     139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |::|||| |::||||
120 GNKWAMDYWGHGASVTVSS 138
                                                                                                                                                                                                                                                                               ;Species: Mus musculus (house mouse)
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121 ATATLLDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Exp. Med. 177, 797-809, 1993
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Ig heavy chain precursor V region (Mab 1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0'7-May-1998 #sequence_revision 15-May-1998 #text_change 21-Jan-2000
C;Accession: 545249; 541429
R;Sassano, M.; Repetto, M.; Cassani, G.; Corti, A.
R;Sassano, M.; Repetto, M.; Cassani, G.; Corti, A.
A;Title: PCR amplification of antibody variable regions using primers that anneal to come.
A;Reference number: 545249; MUID:94261453; PMID:8202386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Residues: 26-76, TK', 79-118, 'V', 120-125,'Y', 127-134,'T', 136-140 <SIE>
A.Cross-references: UNIPARC: UP10000114D5B; GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:
A.Cross-references: UNIPARC: UP10000114D5B; GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:
A.S.Experimental source: strain A.J., hybridoma 36-68
A.Note: the sequence was determined from the differentiated gene
A.Note: the sequence was determined from the differentiated genes that hybridize
A.Note: from analysis of the sizes of several other differentiated genes that hybridize
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Acression: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Acression: A94264; A91261; A02028
R;Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.
A;Title: Sometic mutation in genes for the variable portion of the immunoglobulin heavy A;Reference number: A94264; MUID:82152818; PMID:6801765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dominant anti-arsonate idiotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-140 <SIM>A;Cross-references: UNIPROT:P01746; UNIPARC:UPI00000270DA; GB:J00493; NID:g195006; A;Cross-references: UNIPROT:P01746; UNIPARC:UPI00000270DA; GB:J00493; NID:g195006; A;Experimental source: strain A/J, hybridoma 93G7
R;Sidevitz, M.; Gefter, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
Bir. J. Immunol. 12, 1023-1032, 1982
A;Title: The genetic basis of antibody production: the dominant anti-arsonate idiot:A;Reference number: A91261; MUID:83131846; PMID:6186498
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                                                              61 GKSLEWIGDIDPNFDSSSYNQKFKGKATLTVDKSSNTAYMELRSLTSEDTAVYYCARGGF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.6%; Score 535.5; DB 2; Length 138; 72.4%; Pred. No. 7.5e-39;
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A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                    -- PYGMDYWGQGTSVTVSS 137
                                                                                                                                      121 GSGYYFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.6%;
Best Local Similarity 72.4%;
Matches 105; Conservative 1
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A; Residues: 1-138 <SAS>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-59-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0444
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0444
A;Molecule type: mRNA
A;Residues: 1-150 «KAL»
A;Residues: 1-150 «KAL»
A;Residues: 1-150 manunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
C;Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted «MAT»
F;20-117/Domain: variable region «VRG»
F;34-117/Domain: immunoglobulin homology «IMM»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:g220448; PIDN:BAA00213.1; PID. A;Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:g220448; PIDN:BAA00213.1; PID. A;Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F:119/Domain: signal sequence #status predicted <SIG>F:119/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                         PSSULT 9
PS0057

PS0057

PS0057

Graph and precursor V region (PAR) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000

C;Accession: PS0057

R;Yaolte, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.

J; Biochem. 104, 337-343, 1988

A;Title: Biased expression of variable region gene families of the immunoglobulin heavy

A;Reference number: PS0057; MUID:89197817; PMID:2467902
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Pred. No. 1.5e-39;
4; Mismatches 24; Indels
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             FGSGYYFDYWGQGTTLTVSS 139
                                                                            121 YGGSÝÝPDÝWGQGTTLTVSS 140
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Best Local Similarity 78.4's
Matches 109; Conservative
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A, Molecule type: DNA
A, Residues: 1-135 < YAO>
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A Experimental source: cell line F6-3
C;Comment: This protein is an anti-idiotypic antibody which induces an anti-phosphorylch
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-32/Domain: signal sequence #status predicted <SIG>F;3-151/Product: Ig heavy chain V region 4C11 #status predicted <MAT>F;1-130/Domain: immunoglobulin homology <IMM>F;5-130/Domain: immunoglobulin homology <IMM>F;63-67/Region: complementarity-determining 2
F;82-98/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Bxp. Med. 177, 797-809, 1993
;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GKSLEWIGSTNPYIDYTNYKENPKGRATVTVDKSSSTVYMQLNSLTSEDSAVYYCAR-EG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GQGLEWIGYINPGNDYIHYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGWSWIPLFLLSGTAGVHSBVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 MGWSWIFLFLLSGTAGVISQVQLQQSGPELAKPGASVKMSCKASGYRFTDYVMHWVKQSN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGWSFIFLFLESVSAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTNNGINWVKQRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1484; PH1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:131-140/Region: complementarity-determining 3 F:152-166/Domain: C region(fragment) #status predicted <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reference number: PH1482; MUID:93171820; PMID:8436910; Accession: PH1484
number: PL0011; MUID:88142863; PMID:3125424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%; Score 530.5; DB 2; 72.7%; Pred. No. 2.4e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.3%; Score 525.5; DB 2; Best Local Similarity 73.6%; Pred. No. 5.4e-38; Matches 103; Conservative 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ig heavy chain V region (clones X7-3C5 and X7-3C5H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative 14; Mismatches
                                                             A;Molecule type: mRNA
A;Residues: 1-166 <CHE>
A;Cross-references: UNIPARC:UP10000176D3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>A;Cross-references: UNIPARC:UP10000176BA4
A;Experimental source: hybridoma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 FGSGYYFDYWGQGTTLTVSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GFGNSLDYWGQGTSVNVSS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Giusti, A.M.; Manser, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav d for somatic mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR-WD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWD- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGWSPIFLFLISVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GOGLEWIGYINPGNGYIAYNEKFKGKTTLTVDKSSSTAYMQLRGLTSEDSAVHFCARSVY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0012
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1489
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                                                             C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI0000176BA8
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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    mouse (fragment)

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A;Reference number: PH1482; MUID:93171820; PMID:8436910
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                                                                                                                                                                                                                                                                                         70.3%; Score 532.5; DB 1
74.3%; Pred. No. 1.4e-38;
tive 12; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PL0012
Ig heavy chain precursor V region (P6-3)
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species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: FH1489
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
                                                                                                                                                                                                                                                                                                                                                             104; Conservative
                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                         Query Match
Best Local S:
Matches 104
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C;Accession: PH1498
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav d for somatic mutation.
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J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCA-RWD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                         GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR-WD 119
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                                                                                                                                                                                                                                                                                                                             1 MGMSFIFLFLSVTAGVHSEVOLOOSGAELVRAGSSVKMSCKASGYTFTTYGINWVKQRP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (clone X7-4G7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKWSCKASGYTFTSNGINWVKQRP
                                                                                                                                                                                                                                                                                         1 MCWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                   Gaps
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A;Coss.references: UNIPARC:UP10000176BA9
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                21;
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Pred. No. 1.5e-37;
                                                                                                                                                                             Score 521.5; DB
Pred. No. 1.2e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
                                                                                                                                                                       Query Match
68.8%; Score 521.5; 1
Best Local Similarity 74.1%; Pred. No. 1.2e-
Matches 100; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: immunoglobulin V region; immunog
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Cross-references: UNIPARC:UPI0000176BAB
A, Experimental source: hybridoma cell
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Best Local Similarity
Matches 102; Conserv
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PH1493
Ig heavy chain V region (clone PR14-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1493
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav for somatic mutation.
A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1493
A;Accession: PH1493
A;Accession: PH1493
A;Molecule type: mRNA
                                                           Ig heavy chain precursor V region (B1-8) - mouse
N;Contains: Ig heavy chain precursor V region 186-2
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90809; B90809; A22769; A02034; A02036
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, I A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som A;Reference number: A90809; MUID:81234548; PMID:6788376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-117 <1862>
A; Residues: 1-117 <1862>
A; Cross-references: UNIPARC: UPI000017372E
A; Cross-references: UNIPARC: UPI000017372E
A; Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R; Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
BMBO J. 1, 635-640, 1982
A; Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A; Reference number: A90971; MUID: 84236026; PMID: 7188353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 20-119 <DIL.)
A;Cross-treferences: UNIPARC:UPI000002BD97
A;Note: the V region of the BI-8 delta chain, derived as a spontaneous class switch vari
of the mu chain
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: P01751; UNIPARC: UP100000270EB; GB: J00529; NID: 9195114; PIDN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Froduct: Ig kappa chain V region (B1-8) #status experimental <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-124/Region: D segment
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F;125-139/Region: J segment (JH2)
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-139 <B18>
                                                                                                                                                                                                                                                                                                                                A; Accession: A90809
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ference number: PH1482; MUID:93171820; PMID:8436910

somatic mutation

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Giusti, A.M.; Manser, T.
. Exp. Med. 177, 797-809, 1993
;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GOGLEWIGYIHPGKGYIHYSEKFKDKTTLTVDKSSTAYMQLRSLTSEDSAVYLCARSVY 120
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C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                 DB 2; Length 140;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keyworfs: heteroterramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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A;Cross-references: UNIPARC:UPI0000176BA7
A;Experimental source: hybridoma cell
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterocetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
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;Reference number: PH1482; MUID:93171820; PMID:8436910
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72.9%; Pred. No. 1.5e
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Job time : 5.07199 seca
                                                             A;Residues: 1-140 cGUU>
A;Cross-references: UNIPARC:UPI0000176BA3
A;Experimental source: hybridoma cell
C;Genetics:
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71.4%;
Accession: PH1483
Status: translation not shown
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Best Local Similarity
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/11125837

Publication No. US20050266003A1

GENERAL INFORMATION:
APPLICANT: Chang, Chung Nan
APPLICANT: Chang, Chung Nan
APPLICANT: Chen, Pei-Jiun
APPLICANT: Hang, Chiu-Chen
TITLE OF INVERTION: ANTHEODIES
FILE REFERENCE: 13062-011001
CURRENT APPLICATION NUMBER: US/11/125,837
CURRENT APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
PRIOR APPLICATION NUMBER: US 60/569,892
NUMBER OF SEQ ID NOS: 100
NUMBER OF SEQ ID NOS: 100
SOFTWARE FRANKED FOR Windows Version 4.0
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IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, Nobuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/11193512; Publication No. US20050272918A1 GENERI INFORMATION: APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 GSPYYRYDDWGQGTTLTVSS 138
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STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.78;
77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.7
Best Local Similarity 77.1
Matches 108; Conservative
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US-11-125-837-22
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Publication No. US20060024302A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region US-10-504-389A-28
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Sequence 136, App
Sequence 145, App
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APPLICANT: Scott, Andrew
TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
FILE REFERENCE: LUD 5821
CURRENT APPLICATION NUMBER: US/10/504,389A
CURRENT FILING DATE: 2004-08-10
PRIOR APPLICATION NUMBER: PCT/US03/04243
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.1%; Score 577; DB 6; Length 139; Best Local Similarity 83.6%; Pred. No. 4.7e-41; Matches 112; Conservative 7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 137;
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US-11-097-812-136
US-11-097-812-145
                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                           US-10-504-389A-28
Sequence 28, Application US/10504389A
Publication No. US20060045876A1
GENERAL INFORMATION:
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Best Local Similarity 74.84
Matches 104; Conservative
   120
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ORGANISM: Homo sapiens
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   60.0
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US-11-074-373-39
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   454.5
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) ORGANISM: Artificial Sequence FRAIRES : PRATURE: CHERINE OF THE IGHTON GENERAL OF THE IGHTON CONTROL OF THE IGHTON OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON DESCRIPTION OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF THE IGHTON OF 
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 74.8%;
Matches 104; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Indels
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Best Local Similarity 76.1%; Pred. No. 8.5e-38;
Matches 108; Conservative 5; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lawrence, III, Stanton T
REGISTRATION WUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: <Unknown>
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APPLICANT: Kingsman, Susan Mary
APPLICANT: Bebbington, Christopher Robert
APPLICANT: Carrol, Miles William
APPLICANT: Bland, Pelona Margaret
APPLICANT: Bland, Pelona Margaret
APPLICANT: Myers, Kevin Alan
TITLE OF INVENTION: Antibodies
FILE REPERENCE: 674523-2012
CURRENT PELLING DATE: 2002-11.02
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-11-193-512-27
                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
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Usublication No. US20060014222A1
GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GSGYY---FDYWGQGTTLTVSS 139
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LENGTH: 140 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 27
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61 GKSLEWIGRINPNNGVTLYNQKFKDKAILTVDKSSTTAYMBLRSLTSEDSAVYYCARSTM 120
                                                                                                                                                                                                                                                                                                                        61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                         1 MGWSCIILFLVATATGVHSEVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSH 60
                                                                                                                                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.4%; Score 518.5; DB 7; Length 136; Best Local Similarity 72.7%; Pred. No. 3.1e-36; Matches 101; Conservative 13; Mismatches 22; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKAMURA, MASABUMI
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ROGLEWIGAIFPGNGFTSYNOKFKGKATLTVDKSSSTVYMOLRSLTSEDSAVYFCAR
    Length 592;
Score 536; DB 6; Length 59
Pred. No. 4.2e-37;
9; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1990-12-03
PRIOR FILING DATE: 1990-05-20
PRIOR PILING DATE: 1990-05-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-07-20
PRIOR PILING DATE: 1990-11-21
SOFTWARE: PARENT IN VET: 2.1
SEQ ID NOS: 111
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Query Match
67.7%; Score 513; DB 7; Length 412;
Best Local Similarity 69.9%; Pred. No. 2.4e-35;
Matches 100; Conservative 12; Mismatches 27; Indels
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:|| | | |||||::|||||
271 YGSSPPYYAMDCWGQGTSVTVSS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR-WD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GQGLEWIARIYPGTGNTYYNENFKGKATLTABKSSSTAYMQLSSLTSEDSAVYFCARSGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWD- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPBLVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGWSWIFFFLLSGTAGYHCQVQLKQSGAELVRPGASVKLSCKASGYTFTDYYINWVKQRP 60
                                                                                      APPLICANT: Das., Anuk
APPLICANT: Carton, Jill
APPLICANT: Tsui, Ping
TITLE OF INVENTION: ANTI-MCP1 ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CENSO68
CURRENT APPLICATION NUMBER: US/11/170,453
CURRENT PILING DATE: 2005-06-29
NUMBER OF SEQ ID NOS: 17
SOPTWARE: Patentin version 3.3
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
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US-11-116-939-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-116-939-10

Sequence 10, Application US/11116939

Publication No. US2005026595A1

GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson
APPLICANT: Stephen Tomlinson
APPLICANT: Stephen Tomlinson
FILE OF INVENTION: TISSUE TRREFEED
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT FILING DATE: 2005-04-28
PRIOR PILING DATE: 2005-04-28
PRIOR FILING DATE: 2004-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.4%; Score 518.5; DB 7; Length 1 Best Local Similarity 70.4%; Pred. No. 3.2e-36; Matches 100; Conservative 15; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 293
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121 TVVGNYYGMDYWGQGTSVTVSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --FGSGYYFDYWGQGTTLTVSS 139
                           Sequence 7, Application US/11170453 Publication No. US20060039913A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Mus sp. US-11-170-453-7
                                                                                                                                                                                                                                                                                                                                         142
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR-WD 119
RESULT 9
US-11-116-939-12
Sequence 12. Application US/11116939
Publication No. US200626595A1
GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson
APPLICANT: Richard J. Quigg
TITLE OF INVENTION: TISSUE TARGETED COMPLEMENT MODULATORS
FILE REPRENCE: 1913.0115.0
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT APPLICATION NUMBER: US/11/116,939
PRIOR APPLICATION NUMBER: 00/565,907
PRIOR APPLICATION NUMBER: 00/565,907
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 412
TYPE: PRI
TYPE: PRI
TYPE: PRI
TYPE: RIFORMATION: Description of Artificial Sequence; note=synthetic
GTHER INFORMATION: construct
US-11-116-939-12
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US-11-116-939-11
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Sequence 11, Application Woll116939
Publication No. US2005026595A1
GENERAL INFORMATION:
APPLICANT: Stephen Tomlinson
APPLICANT: Stephen Tomlinson
APPLICANT: Stephen Tossus TARGETED COMPLEMENT MODULATORS
TITLE OF INVENTION: TISSUS TARGETED COMPLEMENT MODULATORS
FILE REFERENCE: 19113.0115U2
CURRENT APPLICATION NUMBER: US/11/116,939
CURRENT APPLICATION NUMBER: 06/565,907
PRIOR FILING DATE: 2004-04-28
PRIOR FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 824
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67.7%; Score 513; DB 7; Length 824;
Best Local Similarity 69.9%; Pred. No. 4.4e-35;
Matches 100; Conservative 12; Mismatches 27; Indels
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                   61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: TIO, MIKITO
APPLICANT: TO, MIKITO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, VOKO
APPLICANT: HANAI, VOKO
APPLICANT: SHIBUYA, WASABUMI
ITILE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
ITILE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR PLILOR DATE: 1999-02-20
PRIOR PLILOR DATE: 1999-02-20
PRIOR PLLING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR PLILOR DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/JD97/04259
PRIOR PLILOR DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PATENTING DATE: 1309-11-21
NUMBER OF SEQ ID NOS: 111
SEQ ID NO 91
LENGTH: 136
TWOFF: DATE
                                                1 MEWSWIFLFLLSGTAGVHSEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYVIHWVRQAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGFSRIFLFFLISVTTGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFINYNMHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein US-11-250-411-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
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                                                                                                                                                                                                      121 GSGYY---FDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                         119 GIRYYGLLGDYWGQGTLVTVSS 140
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Publication No. US20060034838A1
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                                                                                                                                   211 AKSLEWIGVISTYYGHTHYNQKFKGKATLTVDKSSNTAYMELARLTSEDSAIYYCARPNN 270
                                             151 MGWSCVMLFLVATATGVHSQVQLEQSGPELVRPGVSVKISCKGSGYTFTDYAIHWVKQSH 210
                                                                                                     61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCAR-WD 119
1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HANNI, Nobuo
TAKAISU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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69.0%; Pred. No. 3.7e-35;
iive 14; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct.2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY.1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-11-193-512-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                120 FGSG---YYPDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/11193512
Publication No. US20050272918A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAKAMURA, Kazuyasu
IIDA, Akihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANAZAWA, Hideharu
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.01
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                       TYPE: PRT

CRGANISM: Mus musculus
US-11-183-205-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NGOBE 'LECENTOLOGIES', INC.
APPLICANT: DeFrees, Shawn
APPLICANT: ZOPÉ, David
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-US01
CURRENT PEPLICATION NUMBER: US/11/183,205
PRIOR APPLICATION NUMBER: US 60/334,233
PRIOR FILING DATE: 2005-07-15
PRIOR APLICATION NUMBER: US 60/334,301
PRIOR PILING DATE: 2001-11-28
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-05
PRIOR PILING DATE: 2002-06-05
PRIOR PILING DATE: 2002-06-05
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
PRIOR PILING DATE: 2002-08-08
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PRIOR PILING DATE: 2002-08-08
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                                                                                          CURRENT APPLICATION NUMBER: US/11/250,411
CURRENT FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR PILING DATE: 1990-12-03
PRIOR PILING DATE: 1990-05-20
PRIOR FILING DATE: 1990-07-20
PRIOR FILING DATE: 1998-07-20
PRIOR FILING DATE: 1998-07-20
PRIOR PILING DATE: 1998-07-20
PRIOR PILING DATE: 1997-11-21
SOFTWARE: PATENTING DATE: 1997-11-21
SOFTWARE: PATENTING DATE: 1997-11-21
SOFTWARE: PATENTING DATE: 1997-11-21
SOFTWARE: PATENTING DATE: 1997-11-21
SOFTWARE: PATENTING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 62, Application US/11183205
Publication No. US20060030521A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.9
nes 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-183-205-62
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Matches
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWD- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTY 120
                                                                                                                                                                                                                                                                                                                                         1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                             65.2%; Score 494.5; DB 7;
68.6%; Pred. No. 3e-34;
tive 15; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lawrence, III, Stanton T
REGISTRATION WUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MX-1197
APPLICATION NUMBER: US/08/836,561
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
PRIOR FILING DATE: 2002-10-09
PRIOR PEDLICATION NUMBER: US 10/287,994
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
SEQ ID NO 62
LENGTH: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/11193512
Publication No. US20050272918A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 FGSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YGGDWYFNVWGAGTTVTVSA 140
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IIDA, Akihiro ANAZAWA, Hideharu

KOIKE, Masamichi

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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QRPGHDLEWIGYINPSSGYSDYNQSFKGKTTLTADKSSNTAYMQLNSLTSEDSAVYYCAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 QSHGKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCA- 116
                                                                                                                                                                                                                                                                                                                                                                                                          1 MEWSWIFLFLLSGTAGVHSEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYVIHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MINWIWITVFCLLAVAPGAHSAMAQVQLQQSGAELARPGASVKMSCKASGYTFTTYTIHWVR 60
                                                                                                                                                                                                                                                                                                                                                             1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGWSWIFLFLLSGTAGVHS----EVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVK
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45, Application US/10504389A

Publication No. US20060045876A1

GENERAL INFORMATION:

APPLICANT: Scott, Andrew

TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC

TITLE OF INVENTION: ANTIBODIES AND USES THEREOF

FILE REFERENCE: LUD 581.

CURRENT FILING DATE: 2004-08-10

PRIOR APPLICATION NUMBER: PCT/US03/04243

PRIOR FILING DATE: 2002-02-12

NUMBER OF SEQ ID NOS: 56
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2
                                                                                                                                                                                                                                                                   Length 140;
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                                                                                                                                                                                                                                                              Query Match 65.1%; Score 493.5; DB 7; Length 1 Best Local Similarity 67.6%; Pred. No. 3.6e-34; Matches 96; Conservative 14; Mismatches 27; Indels
                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 74:

95-11-193-512-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GSGYY---FDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIRYYGLLGDYWGQGTLVTVSS 140
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                                                                          LENGTH: 140 amino acids
                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 74
                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.9
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 45
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEWSWIFLFFLLSGTAGVHSEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYVIHWVRQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 140;
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTURARE: PERISEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIPICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
                                                                                        Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/08/05.561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.3%; Score 487.5; Best Local Similarity 66.9%; Pred. No. 1.1 Matches 95; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GSGYY---FDYWGQGTTLTVSS 139
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                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR
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Sequence 83, Application US/11193512
Publication No. US20050272918A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
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TELEPKX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 140 amino acids
TYPE: amino acid
                                     118 GQG----YWGQGTLVTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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121 GSGYYFDYWGOGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 95; Conserva
                                                                                                                                  US-11-193-512-83
                                                                                                             RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARW-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGWSYIILFLVATATEVHSQVQLQQSGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
64.2%; Score 487; DB 6; Length 143;
Best Local Similarity 68.5%; Pred. No. 1.3e-33;
Matches 98; Conservative 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY FILE REFERENCE: A6689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT APPLICATION NUMBER: US/10/729,441
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR PILING DATE: 2003-12-08
PRIOR FILING DATE: 2003-10/170,390
PRIOR FILING DATE: 2003-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE PLEATION NOS: 96
SOFTWARE PLEATION VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 4.8e-33; 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POUL ANGEW HAMBLING APPLICANT: Paul Alexander WILSON APPLICANT: Paul Alexander WILSON APPLICANT: Alan Peter LEWIS TITLE OF INVENTION: IMMUNOGLOBULINS FILE REFERENCE: PB60608-2 CURRENT PLING DATE: 2005-07-06 PRIOR APPLICATION NUMBER: PCT(BE2004/005325 PRIOR FILING DATE: 2004-12-22 PRIOR FILING DATE: 2003-12-22 NUMBER OF SEQ ID NOS: 113 SOFFWARE: FREUESQ for Windows Version 4.0 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.1%; Score 485.5; 69.1%; Pred. No. 4.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DYYGSSKWYFDVWGAGTTVTVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 DF--GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/11177648 Publication No. US20060029603A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jonathon Henry ELLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 69.19
Matches 96, Conservative
    APPLICANT: ImmunoGen, Inc.
                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Mus musculus US-10-932-334-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapien
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEWSWIFLFLLSGTAGVHSEVQLVQSGAEVKKPGASVKVSCKASGYTFTSYVIHWVRQRP
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                                                                                      TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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; Pred. No. 2.9e-33;
12; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 7005-115-999
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PSSLENG Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: US/10/283,349
APPLICATION NUMBER: US/10/283,349
                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: UP 232384/95
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-11-193-512-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, Nobuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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us-10-687-035-34.rapbn

Mon Mar 20 08:49:45 2006

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121 GSGYY---FDYWGOGTTLTVSS 139

Search completed: March 20, 2006, 07:32:42 Job time: 2.60454 secs

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Result No.

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US-10-257-864A-88
US-10-251-111-93
US-10-399-518-117
US-10-399-565-117
US-10-645-085A-88
US-10-642-120-2
US-10-642-122-2
US-10-642-122-2
US-10-642-122-2
          |S-10-828-782A-18
|S-10-500-696-2
|S-10-138-505-12
|S-10-257-864A-88
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US-10-723-003-46
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                                                                           March 20, 2006, 07:31:52; Search time 24.6746 Seconds (without alignments) 2353.772 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                   ......FGSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
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(gn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
            GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-903-327A-13
-09-903-327A-12
-09-903-327A-11
-09-903-327A-14
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-159-006-30
US-10-462-062-157
                                                                                                                                                                                                           1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                          US-10-687-035-34
758
1 MGWSWIFLFLLSGTAGVHSE.
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Maximum DB seq length: 200000000
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                     Copyright
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Match
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                                                                                                                           Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: 776.1 heavy chain polypeptide variable region (776.1H)
US-10-687-035-34
                                                                                                              Sequence 34, Application US/10687035

Publication No. US20050064518A1

SERREAL INFORMATION:
APPLICANT: ANDONE, Earl F.
TILLE OF INVENTION: ANTIBODES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODES THAT BIND CELL-ASSOCIATED
TITLE OF INVENTION: ANTIBODES: 00,10,687,035
CURRENT FILING DATE: 2003-00-15
PRIOR APPLICATION NUMBER: 60/485,986
PRIOR APPLICATION NUMBER: 60/486,986
PRIOR PILING DATE: 2003-10-12
PRIOR PILING DATE: 2003-10-12
PRIOR FILING DATE: 2003-10-12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
FURNEL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:
Co. Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coelingh, Kathleen L.
Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 758; DB 5; 100.0%; Pred. No. 4.4e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GSGYYFDYWGQGTTLTVSS 139
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 139; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-389-155-60
                                                                            RESULT 1
US-10-687-035-34
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1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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82.5%; Score 625; DB 4; Length 135;
Best Local Similarity 84.9%; Pred. No. 2.3e-47;
Matches 118; Conservative 7; Mismatches 10; Indels
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Schneider, William P.
Landolfi, Nicholas F.
Coelingh, Kathleen L.
Selick, Harold B.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 011823-002650US TELECOMMUNICATION INFORMATION:
                  PRELICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
PRIOR APPLICATION DATA: 2003
FILING DATE: 0.-JUN 1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/531,278
FILING DATE: 10-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 10-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: WILLIAM M.
REGISTRATION NUMBER: 30,233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-389-155-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0200
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Publication No. US20040049014A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GSGYYFDYWGQGTTLTVSS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Queen, Cary L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 60
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CURRENT APPLICATION
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ORGANISM: Artificial Sequence
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84.9%;
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Best Local Similarity 84.9
Matches 118; Conservative
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APPLICANT: Occasion Sung
APPLICANT: Co, Man Sung
APPLICANT: Co, Man Sung
APPLICANT: Schneider, William
APPLICANT: Schneider, William
APPLICANT: Selick, Marchleen
APPLICANT: Selick, Harold
TITLE OF INVENTION: Improved Humanized Immunoglobulins
FILE REFERENCE: 05882.0078.CNUS01
FILE REFERENCE: 05882.0078.CNUS01
CURRENT PAPLICATION NUMBER: 09/718,993
FRIOR PRILING DATE: 1095-06-07
FRIOR PELLING DATE: 1995-06-07
FRIOR PELLING DATE: 1995-06-07
FRIOR PELLING DATE: 1995-12-19
FRIOR PLILING DATE: 1990-12-19
FRIOR PLILING DATE: 1990-12-19
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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Pred. No. 2.3e-47;
7; Mismatches 10;
                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/310, 252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
FILING DATE: 07-JUN-1995
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,417
                                                                                                                                     APPLICATION NUMBER: US/09/325,000
                                                                                                                                                         FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-389-417-60
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                 FILING DATE: 13-Mar-2003
CLASSIFICATION: <Unknown>
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Publication No. US20040058414A1
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Best Local Similarity 84.9%;
Matches 118; Conservative
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| GENERAL INFORMATION:
| APPLICANT: SATO, KOH
| APPLICANT: ADACH! HIDEKI
| APPLICANT: ADACH! HIDEKI
| APPLICANT: ADACH! HIDEKI
| TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
| TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
| FILE REFERENCE: 053466-0360
| CURRENT PELING DATE: 2003-06-16
| PRIOR APPLICATION NUMBER: PCT/JD99/01768
| PRIOR APPLICATION NUMBER: UP 10-91850
| PRIOR APPLICATION NUMBER: UP 10-91850
| PRIOR APPLICATION NUMBER: UP 10-91850
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| PRIOR APPLICATION NUMBER: UP 10-91850
| PRIOR FILING DATE: 1998-04-03
| SOFTWARE: PALEMENT PLING DATE: 137
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OTHER INFORMATION: Description of Artificial Sequence: Full-length amino action of The Sequence for H chain V region of anti-TF mouse monoclonal OTHER INFORMATION: antibody ATR-2
US-10-462-062-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 625; DB 4;
Pred. No. 2.3e-47;
7; Mismatches 10
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US-10-452-357-69
PRIOR FILING DATE: 1989-02-13
PRIOR APPLICATION NUMBER: 07/290,975
PRIOR FILING DATE: 1988-12-28
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.2
SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 153, Application US/10462062 Publication No. US20040044187A1
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Mon Mar 20 08:49:45 2006

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6; Mismatches
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Publication No. US200502026A1
GENERAL INFORMATION:
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Best Local Similarity 83.5%;
Matches 116; Conservative
   Matches 116; Conservative
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US-10-781-989-14
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Publication No. US20040044187A1

Publication No. US20040044187A1

APPLICANT: NORMATION:

APPLICANT: AATO, KOH

TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMANIZED ANTIBODIES

FILE REPERENCE: 053466-0360

CURRENT FILING DATE: 2003-06-16

PRIOR PILING DATE: 1999-04-02

PRIOR PLING DATE: 1999-04-02

PRIOR PLING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE PARENCE: PRIOR IN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFICE TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN OFFI TOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEMSWIFLFLLSGTTGVHSEIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 613.5; DB 3; Length 132; Pred. No. 2.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
81.3%; Score 616; DB 4; Length 137;
Best Local Similarity 82.7%; Pred. No. 1.4e-46;
Matches 115; Conservative 8; Mismatches 14; Indels
GEGYYFDYWGQGTTLTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGYYFDYWGQGTTLTVSS 139
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ORGANISM: Artificial Sequence
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ORGANISM: Unknown Organism
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Best Local Similarity
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Sequence 6, Application US/09903327A

Batent No. US20020164333A1

GENERAL INFORMATION

APPLICANT: Nomerow, Glen R.

APPLICANT: Li, Erguang

TITLE OF INVENTION: BENUT

TITLE OF INVENTION: DELIVERY

TITLE OF INVENTION: DELIVERY

TITLE OF INVENTION: US/09/903,327A

CURRENT FILING DATE: 2001-07-10

FRIOR PELLING DATE: 2000-07-10

RECORDER FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HIATT, Andrew C.
APPLICANT: HIATT, MA, Julian K.-C.
APPLICANT: HIATT, MA, Julian K.-C.
APPLICANT: LEHNER, Thomas
TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOCLOBULINS
TITLE OF INVENTION: CONTAINING PROTECTION PROTEINS IN PLANTS AND THEIR USE
FILE REFERENCE: 415142000303
CURRENT PELING DATE: 2004-02-18
FRIOR PELING DATE: 1995-05-04
FRIOR APPLICATION NUMBER: 08/434,000
FRIOR FILING DATE: 1995-05-04
FRIOR PILING DATE: 1994-12-30
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 14
LENGTH: 132
TYPE: PRT
                                                                                                                                                                              61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                           1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
  7; Gaps
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10; Indels
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Pred. No. 2.3e-46;
6; Mismatches 10;
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APPLICANT: Li, Erguang
TITLE OF INVENTION: BIPUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETIF
TITLE OF INVENTION: GENB
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
RIGHT APPLICATION NUMBER: US/613,017
RIGHT APPLICATION NUMBER: US/613,017
RIGHT FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PARTENER PARTENER OF SEQ ID NOS: 33
LENGTH: 493
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Sequence 12, Application US/09903327A

Patent No. US2002016433A1

GENERAL INFORMATION:

APPLICANT: Nemerow, GIB R.

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETS

TITLE OF INVENTION: DELIVERY

TITLE OF INVENTION: DELIVERY

FILE REPERRACE: 22908-1228

CURRENT APPLICATION NUMBER: US/09/903,327A

CURRENT APPLICATION NUMBER: 09/613,017

PRIOR RILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

SOFTHER SECTION NUMBER: 09/613,017

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

LENGTH S. SOFTHER SECTION NUMBER: 09/613,017

BRION PILING DATE: 2000-07-10

SEQ ID NO 12

LENGTH S. SOFTHER SECTION NUMBER: 09/613,017

LENGTH S. SOFTHER SECTION NUMBER: 09/613,017

LENGTH S. SOFTHER SECTION NUMBER: 09/613,017

LENGTH S. SOFTHER SECTION NUMBER: 09/613,017

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LENGTH S. SOFTHER SECTION NUMBER: 09/613,017

LENGTH S. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
FOTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
FOTHER INFORMATION: and IGF-1 mature peptide
US-09-303-327A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.2%; Score 600.5; DB 3; Length 493; Best Local Similarity 82.0%; Pred. No. 1.3e-44; Matches 114; Conservative 6; Mismatches 12; Indels 7;
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                                                                                Sequence 13, Application US/09903327A Patent No. US20020164333A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GSGYYPDYWGQGTTLTVSS 139
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 82.09
Matches 114; Conservative
                                                                                                                                                                                                        APPLICANT: Nemerow, Glen R. APPLICANT: Li, Erguang
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Patent No. US20020164333A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION: DELIVERY
TITLE OF INVENTION NUMBER: 09/913,327A
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKSLEWIGYIYPYKGGTGYNQKFKSKATLITDSSSNTAYMELRSLTSDASAVYYCARG-- 118
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                                                                                                                                                                                                                                                                                LOCATION: (0) ...(0)
COTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
COTHER INFORMATION: Difunctional antibody
US-09-903-327A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGWSWIPLFLLSGTAGVHSEVQLQQSGPELVXPGASVKISCKASGYTFTDYNIHWVKQSH
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CTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody US-09-903-327A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.2%; Score 600.5; DB 3; Length 9 Best Local Similarity 82.0%; Pred. No. 1.2e-44; Matches 114; Conservative 6; Mismatches 12; Indels
SOPTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GSGYYFDYWGQGTTLTVSS 139
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ORGANISM: Mouse
                                                                                                                                                                 ORGANISM: Mouse
                                                                                                                       TYPE: PRT
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FEATURE: OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain OTHER INFORMATION: and SCF mature peptide
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APPLICANT: The director of Chubu National Hospital
APPLICANT: The director of Chubu National Hospital
APPLICANT: STIBATA, Masao
APPLICANT: SHIBATA, Masao
ITILE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
ITILE OF INVENTION: Amtibody recognizing GM1 ganglioside-bound
ITILE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
ITILE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
ITILE OF INVENTION: Application NUMBER: US/10/768,193
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 16
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
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                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                  Query Match 79.2%; Score 600.5; DB 3; Length 613; Best Local Similarity 82.0%; Pred. No. 1.7e-44; Matches 114; Conservative 6; Mismatches 12; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 585.5; DB 4;
Pred. No. 6.9e-44;
7; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10774076; Publication No. US20040210040A1
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Publication No. US20040181042A1
GENERAL INFORMATION:
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                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 79.9
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Mus musculus
US-10-768-193-7
                                                                                                                                                                         US-09-903-327A-14
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SEQ ID NO 14
LENGTH: 613
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Batent No. US30020164333A1

GENERAL INFORMATION:
APPLICANT: Li, Erguang
TITLE OF INVENTION: BEFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: BELIVERY
FILE REFERENCE: 22908-1228
CURRENT PAPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Li, Erquang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22008-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 11
LENGTH: 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain ; OTHER INFORMATION: and TNF alpha mature peptide US-09-903-327A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GKSLEWIGYIYPYKGGTGYNQKFKSKATLTTDSSSNTAYMELRSLTSDASAVYYCARG-- 118
                                                                                                    61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                     1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYFFTDYNMHWVKQSH
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79.2%; Score 600.5; DB 3; Length
Best Local Similarity 82.0%; Pred. No. 1.6e-44;
Matches 114; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09903327A, Patent No. US20020164333A1, GENERAL INFORMATION: APPLICANT: Nemerow, Glen R.
                                                                                                                                                                                                                                  |||||| :||||
----IAYWGQGTLVTVSA 132
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                                                                                                                                                                                                      121 GSGYYFDYWGQGTTLTVSS 139
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US-09-903-327A-14
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US-09-903-327A-11
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; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region US-10-365-123-28
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolfi, et al.
TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and TITLE OF INVENTION: Papplicanis
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKSLEWIGYIDPYYGDPGYSQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCARRG- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEWRWIFLFLISGTTGVHSEIQLQQSGPELVKPGASVKVSCKASGYAFTNYNWYWQGH 60
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; Publication No. US20040053365A1
; GENERAL INFOMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Burgess, Andrew
; APPLICANT: Burgess, Andrew
; TITLE OF INVENTION: HUMANIZED
; CURRENT APPLICATION NUMBER: US/10/365,123
; CURRENT FILING DATE: 2003-02-12
; UNDMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 578.5; DB 4
Pred. No. 2.9e-43;
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Best Local Similarity 79.1%;
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: mus sp.
US-10-774-076-9
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RESULT 18 US-10-462-062-158

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OTHER INFORMATION: Description of Artificial Sequence: Full-length amino actioned in OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal COTHER INFORMATION: antibody ATR-8
US-10-462-062-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GKSLEWIGYIDPYTGGTGYNOKFNDKATLTVDKSSSTAFWHLNSLTSEDSAVYYCAR--- 117
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.9%; Score 568; DB 4; Length 137; Best Local Similarity 75.4%; Pred. No. 2.4e-42; Matches 107; Conservative 11; Mismatches 16; Indels
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ZIP: 20007-5100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                              TITLE UF INVESTIGATION TAND FACALLY OF THE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR PILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 158
LENGIH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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APPLICATION NUMBER: US/10/837,904
FILING DATE: 04-May-2004
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TSUCHIYA, Masayuki
SATO, Koh
BENDIG, Mary Margaret
JONES, Steven Tarran
SALDANHA, JOSE WILLIAM
TITLE OF INVENTION: RESHAPED HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 134
CORRESPONDENCES ADDRESS:
ADDRESSER FOLEY & LABDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 --GFYYDYDCYWGQGTLVTVSA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 567; DB 5; Length 135;
Pred. No. 2.9e-42;
8; Mismatches 18; Indels
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Schneider, William P.
Landolfi, Nicholas F.
Coelingh, Rathleen L.
Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                  PILING DATE: 13-Jul-1998
APPLICATION NUMBER: US 08/436,717
FILING DATE: 08-MAY-1995
APPLICATION NUMBER: US 08/137,117
APPLING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
                                                                                                                                           FILING DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/POCKET NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003
US/09/114,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 72, Application US/10389155
Publication No. US20030229208A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.8%;
78.4%;
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.8
Best Local Similarity 78.4
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-389-155-72
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GONLEWIGLINPYNGGTSYNOKFKGKATLTVDKSSNTAYMELLSLTSADSAVYKCTRRGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 138;
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.6%; Score 565.5; DB 78.4%; Pred. No. 4.1e-42
AFLING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FBB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-389-155-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        completed: March 20, 2006, 07:35:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 -RDYSMDYWGQGTSVTVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.43
Matches 109; Conservative
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

March 20, 2006, 07:30:27; Search time 7.40237 Seconds (without alignments) 1552.466 Million cell updates/sec

US-10-687-035-34 758 1 MGWSWIFLFLLSGTAGVHSE......FGSGYYFDYWGQGTTLITVSS 139 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

572060 segs, 82675679 residues Searched:

572060 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Issued\_Patents\_AA:\* Database :

/cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |                          |            | Appl            | Appl             | Appl             | Appl             | Appl             | , App            | , App             | Appl              | Appl            | Appl             | Appli            | Appli           | Appl              | Appli            | Appli           | Appl             | , App             | Appl             | Appl            | Appli           | Appl             
|-----------|--------------------------|------------|-----------------|------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|-----------------|------------------|------------------|-----------------|-------------------|------------------|-----------------|------------------|-------------------|------------------|-----------------|-----------------|------------------|------------------|------------------|------------------|------------------|------------------|-----------------|
|           | ş                        | = :        | 69              | 69               | 69               | 69               | 69               | 153,             | 154,              | 14,               | 14,             | 14,              | ٦<br>٦           | 7               | 91,               | 3                | 'n              | 93,              | 158,              | 27,              | 27,             | 4               | 85,              | 85,              | 82,              | 85,              | 85,              | 26,              | 30,             |
|           | 40,140,000               | DEBCITOCIO | Sequence        | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence          | Sequence          | Sequence        | Sequence         | Sequence         | Sequence        | Sequence          | Sequence         | Sequence        | Sequence         | Sequence          | Sequence         | Sequence        | Sequence        | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence         | Sequence        |
| Ø         |                          |            | 18-69           | 28-69            | 40-69            | 69-00            | 37-69            | 68-153           | 68-154            | 00A-14            | 57-14           | 88-14            | 78E-1            | 62-1            | 28B-91            | 78E-3            | 62-3            | 28B-93           | 68-158            | 17D-27           | 17-27           | 612-4           | 78-85            | 28-85            | 40-85            | 00-85            | 37-85            | 93-26            | 93-30           |
| SUMMARIES |                          |            | 34-2            | 7-77             | 74-0             | 87-2             | 84-5             | 4-4              | 47-4              | 34-0              | 12-1            | 17-8             | 16-7             | 38-5            | 83-5              | 16-7             | 38-5            | 83-5             | 47-4              | 37-1             | 36-7            | 3-11            | 34-2             | 77-7             | 74-0             | 87-2             | 84-5             | 01-5             | 01-5            |
| SUMM      | £                        | 1          | US-07-634-278-6 | US-08-477-728-69 | US-08-474-040-69 | US-08-487-200-69 | US-08-484-537-69 | US-09-647-468-15 | US-09-647-468-154 | US-08-434-000A-14 | US-09-312-157-1 | US-09-717-888-14 | US-08-116-778E-1 | US-08-438-562-1 | US-08-483-528B-91 | US-08-116-778E-3 | US-08-438-562-3 | US-08-483-528B-9 | US-09-647-468-158 | US-08-137-117D-2 | US-08-436-717-2 | PCT-US93-11612- | US-07-634-278-85 | US-08-477-728-85 | US-08-474-040-85 | US-08-487-200-85 | US-08-484-537-85 | US-09-301-593-26 | US-09-301-593-3 |
|           | 9                        | 9 !        | н               | ٦                | ч                | ч                | 7                | ~                | 7                 | ~                 | 7               | 7                | -                | Н               | -                 | ٦                | Н               | -4               | ~                 | -                | -               | 4               | Н                | -                | ч                | -                | ~                | ~                | 7               |
|           | Query<br>Match Length DB |            | 135             | 135              | 135              | 135              | 135              | 137              | 137               | 132               | 132             | 132              | 139              | 139             | 139               | 137              | 137             | 137              | 137               | 135              | 135             | 140             | 138              | 138              | 138              | 138              | 138              | 143              | 472             |
| d         | Query                    | ייים רכזו  | 82.5            | 82.5             | 82.5             | 82.5             | 82.5             | 81.3             | 81.3              | 80.9              | 80.9            | 80.9             | 79.7             | 79.7            | 79.7              | 77.3             | 77.3            | 77.3             | 74.9              | 74.8             | 74.8            | 74.7            | 74.6             | 74.6             | 74.6             | 74.6             | 74.6             | 74.4             | 74.4            |
|           | 3000                     | 3000       | 625             | 625              | 625              | 625              | 625              | 616              | 616               | 613.5             | 613.5           | 613.5            | 604              | 604             | 604               | 586              | 586             | 286              | 268               | 267              | 567             | 566.5           | 565.5            | 565.5            | 565.5            | 565.5            | 565.5            | 564              | 564             |
|           | Result                   | 2          | -               | 7                | m                | 4                | S                | 9                | 7                 | ω                 | σ               | 10               | 11               | 12              | 13                | 14               | 15              | 16               | 17                | 18               | 19              | 20              | 21               | 22               | 23               | 24               | 25               | 56               | 27              |

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Appl Appl Appl Appl	Appl Appl Appl App	Appl Appli Appli	Appli App	Appli Appli Appli	Appl Appl	Appl	Appl Appl	Appli Appli	Appli Appli	Appli Appli	Appii Appi	App App	Appli Appli	Appl Appl	Appl Appl	Appl Appli	Appli Appli	Appli Appli	Appl	Appli	Appli	Appl Appl	Appl Appl	App1	Appl	Appl	Appl Appli	Appli	Appli Appli	App1	Appli Appli
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-644-33 -246A-33 -644-19 -644-28 -644-42	-246A- -246A- -246A- -468-1	-5/64-1 -644-1 -246A- -194-8	-724-8 -3858-11 -752-112	-057-18 -419-2 -539A-4	-561- -122- -278-	-728-1 -040-1	-569B-	-682-4 -914-4	-710A	66,	-690-3 11611-1	-468-	-940-4 -692-6	-278-	-040-5	-537-5	-569B-	-515-	-421-	-586-8	-024-2	-882-78	-1130	-932-7	-017-7	-561-6	-122-6. -284-4	-939-	-164A-4		-520-7 05262-
40444	00000	S-08-23 S-08-23 S-08-23	S-09-26 S-09-26 S-09-39	S-08-37 S-08-39 S-08-39	S-08-83 S-09-43 S-07-63	S-08-47	S-08-30 S-08-30 S-08-48	S-08-83 S-08-89	S-09-35 S-09-35	S-09-35 S-08-20	S-08-96 CT-US93	S-09-64 S-09-64	S-08-57 S-08-83	S-07-63 S-08-47	S-08-47 S-08-48	S-08-48 CT-US91	S-08-30 S-08-11	S-09-79	S-07-94	S-08-65	S-08-60 S-08-60	S-08-48	S-08-48 S-08-47	S-08-48 S-08-72	5-08-71	5-08-83	S-09-43 S-08-46	5-08-46	5-08-45	S-08-13 S-08-43	S-08-23 CT-US95
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233 233 235 235 235	<b>~~~~~~</b>	* ** ** **	444	. പെ പ	446	999	า๛๛	നന	9	66	m m		44	-		19	99	99	***	100	200	າຕ	m m	mm	~ ~	. 4	* *	47.5	* **	mm	44 44
73.9 73.9 9.87 9.87 9.87	73.9 73.9 73.9	1 00 00 01	404		000	000	00	99	$\sigma \sigma$	69.3 69.1					œ œ	e e	67.7				: : .				6.4			· ·			
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28 30 31 32	6 4 12 9 t	J W W 4 4	. 4 4 4 4 5 6 4	2 4 4 2 4 5 5 4 5	4 4 7 8 0 C	22 22	5 4 S	56 57	5.58 9.00	61	63 62	65 65	67	69 69	27 1.7	72	74	76	78	86	85	9 60 2 4	8 8 9 2	8 8 8	6 6	91	9 9 8	4 0	0 0 0 0	98	100

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RESULT 3
RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMDVRSLTSEDSAVYYCAR--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSWIFLFRILSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 625; DB 1; Length 135;
Pred. No. 2e-57;
7; Mismatches 10; Indels
                                                                                                                                                                                               APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harchleen L.
APPLICANT: STUTELE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: 379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PASADALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PED PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: A24
PRICA STRICATION DATA:
APPLICATION NUMBER: US 07/590,274
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
PRICA PAPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
FILING DATE: 13-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WIlliam M
REGISTRATION NUMBER: 30,223
REFERENCE/COCKET NUMBER: 31,23-302600
TELEDEPHONE: (415) 326-2400
ALIGNMENTS
                                                                                                                          ; Sequence 69, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||::|||||
118 -GRPAMDYWGQGTSVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 84.9%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-07-634-278-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94301
                                                                             RESULT 1
US-07-634-278-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH
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82.5%; Score 625; DB 1; Length 135;
Best Local Similarity 84.9%; Pred. No. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels
Sequence 69, Application US/08477728

Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OFFRAINGS STSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: O'-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION TATA:
APPLICATION NUMBER: US/034,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
PRIOR APPLICATION NUMBER: US 07/590,274
PRIOR APPLICATION NUMBER: US 07/590,274
PRIOR APPLICATION NUMBER: US 07/590,975
PRIOR APPLICATION NUMBER: US 07/310,252
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMICH, MAILIAM M
REGISTENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
THE FORMATION INFORMATION:
                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto COUNTRY: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 -GRPAMDYWGQGTSVTVSS 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-477-728-69
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APPLICANT: COLANT: COLANT: COLANT: COLANT: COLANT: COLANT: COLANT: COLANT: APPLICANT: SCHNEIDER, William P.
APPLICANT: SCHNEIDER, Wicholas F.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew CITY: Palo Alto
STREE: Alfornia
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.25
SOCTAMEN: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1999
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: REPEL-108
APPLICATION NUMBER: US 07/290,975
FILING DATE: 38-DEC-1989
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: APPLICATION NUMBER: 11823-002610
TELERCOMMUTCATION INFORMATION:
NAME: Smith, William M
REFERENCE/DOCKET NUMBER: 11823-002610
TELERCOMMUTCATION INFORMATION:
TELERCOMMUTCATION INFORMATION:
TELERCOMMUTCATION INFORMATION:
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TELERCOMMUTCATION INFORMATION:
TELERCOMMUTCATION INFORMATION:
Application US/08487200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INPORMATION FOR SEQ ID NO: 69;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-487-200-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMDVRSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 625; DB 1; Length 13
Pred. No. 2e-57;
7; Mismatches 10; Indels
                                                                                                      APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHWEIDER, William P.
APPLICANT: SCHEIDER, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 1 LBM FC COMPACTORS
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIPICATION: 536
FILING APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/530,274
FILING DATE: 12-DEC-1990
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1999
FILING DATE: 13-FEB-1999
FILING DATE: 13-FEB-1999
FILING DATE: 32-DEC-1988
APPLICATION NUMBER: US 07/290,975
FILING DATE: 326-2400
TELECOMMUNICATION INFORMATION:
ATORNEY/AGENT INFORMATION:
TELEFAK: (415) 326-2400
TELEFAK: (415) 326-2400
TELEFAK: (415) 326-2402
TELEFAK: (415) 326-2402
TELEFAK: TANDER SEQUENCE: TANDER SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend Khourie and Crew 379 Lytton Avenue
                       pplication US/08474040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%;
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Best Local Similarity 84.9
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-474-040-69
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                 1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                             Query Match 82.5%; Score 625; DB 1; Length 13
Best Local Similarity 84.9%; Pred. No. 2e-57;
Matches 118; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 -GRPAMDYWGQGTSVTVSS 135
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RESULT 5 US-08-484-537-69

-GRPAMDYWGQGTSVTVSS 135 121 GSGYYFDYWGQGTTLTVSS 139

118

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RESULT 4 US-08-487-200-69

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121 GSGYYFDYWGQGTTLTVSS 139
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Best Local Similarity 82.7%;
Matches 115; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSWIFLFILLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNM4WVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.5%; Score 625; DB 2; Length 135;
84.9%; Pred. No. 2e-57;
tive 7; Mismatches 10; Indels
                                                                                     APPLICANT: COLMAN SUNG
APPLICANT: COLMAN SUNG
APPLICANT: SCHNETDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: CELINCH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOCLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
RESISTATION NUMBER: 11823-00260
TELECOMMUNICATION NUMBER: 11823-00260
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-647-468-153
; Sequence 153, Application US/09647468
Sequence 69, Application US/08484537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 -GRPAMDÝWĠQĠTSVTVŠŠ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 135 amino acids
amino acid
                                                                    QUEEN, Cary L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82.5
Best Local Similarity 84.9
Matches 118; Conservative
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CHERRIL INFORMATION:
APPLICANT: AND KON!
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APPLICANT: AND KON!
APPLICANT: AND WORDER: 1970, KON!
APPLICANT: AND WORDER: 1970, KON!
APPLICANT: AND WORDER: 1970, MANUAL PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TITLE OF INVESTICE: 192466/0289
PRINTS APPLICATION WORDER: 1970, 1970, 1970
PRINTS APPLICATION WORDER: 1970, 1970
PRINTS APPLICATION WORDER: 1970, 1970
PRINTS APPLICATION WORDER: 1970, 1970
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PRINTS APPLICATION WORDER: 1970
PRINTS APPLICATION WORDER
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81.3%; Score 616; DB 2; Length 137;

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61 GKSLEWIGYIYPYNGNTYYNOKFKNKATLTVDNSSTSAYMELRSLTSEDSAVYYCAT--- 117
                                               61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
  1 MEWIWVPLFLLSGTAGVHSGVQLQQSGPDLVKPGASVKISCKASGYTFTDYNIHWVKQSR 60
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION CURKNOWN>
PRIOR APPLICATION UNMBER: 08/434,000
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 08/434,000
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: GILBG. JOÉTERY W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09312157
Patent No. 6303341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
                                                                                                                                     121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                  118 ----YPDYWGQGTTLTVSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90071
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-312-157-14
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                                                                                                                                                            61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                       61 GKSLEWIGYIDPYNGGTIYNQKFKGKATLTVDKSSSTAFWHLNSLTSEDSAVYYCARG-- 118
                                                                                               1 MEWSWIFLFLLSGTIGVHSEIQLQQSGPELVKPGASVKVSCKASGYSFIDYNMYWVKQSH 60
                                                                    1 MGWSWIFLFFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 613.5; DB 2; Length
Pred. No. 3e-56;
6; Mismatches 10; Indels
                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08434000A
Patent No. 6046037
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOCLOBULINS CONTAINING PR
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR
    Pred. No. 1.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION UNDER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guy's 13 Gamma 1
                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                    GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                               119 GEGYYFDYWGQGTTLTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.5%;
Matches 116; Conservative (
82.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Guise, Jeffrey W. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 67-3510
TELEX: SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
TOPOLOGY: DESCRIPTION:
  Best Local Similarity 82.7
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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61 GKSLEWIGYIYPYNGNTYYNQKFKNKATLTVDNSSTSAYMELRSLTSEDSAVYYCAT--- 117
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                                                                                                                                                                                                                                                                    1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                  7;
                                                                                                                                    Length 132;
                                                                                                                                                                                                  Indels
DESCRIPTION: Guy's 13 Gamma SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                             Query Match 80.9%; Score 613.5; DB 2; Best Local Similarity 83.5%; Pred. No. 3e-56; Matches 116; Conservative 6; Mismatches 10;
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Sequence 1, Application US/08116778E Patent No. 5830470 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-116-778E-1
                                     S-08-116-778E-1
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                                                                                                                                                                                                       APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 613.5; DB 2; Length 132;
Pred. No. 3e-56;
6; Mismatches 10; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: Guy's 13 Gamma 1 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/717,888

FILING DATE: 20-No. 6808709-2000

CLASSIFICATION: -CURROWN>
PRIOR APPLICATION AUTR:

APPLICATION NUMBER: US/08/434,000

FILING DATE: 30-Dec-94

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUICATION INFORMATION:

TELEPHONE: (619) 552-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
                                                                                                                                           Sequence 14, Application US/09717888 Patent No. 6808709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GSGYYFDYWGQGTTLTVSS 139
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121 GSGYYFDYWGQGTTLTVSS 139
                                     118 ----YFDYWGQGTTLTVSS 132
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Best Local Similarity 83.5%;
Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                                   RESULT 10
US-09-717-888-14
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BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD: CONSENSUS (Product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OD: CONSENSUS
/product= "HYPERVARIABLE REGION
                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTOKNEY/AGENT INPORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 32,955
REFERENCE/POCKET UNBER: 249-59
TELECOMMULICATION INFORMATION:
TELEPHONE: (703)816-4000
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HAMAI, NOBUO
APPLICANT: HASEGAMA, WAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                                                                    ADDRESSEE: NIXON & VANDERHYB P.C. STREET: 1100 NORTH GLEBE ROAD CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acide TOPOLOGY: li-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 50..66
IDENTIFICATION METHOD: B
IDENTIFICATION METHOD: WITHOUS WITHOUS WITHOUS WITHOUS WITHOUS WITHOUS WITHOUS WARNERS: A domain
LOCATION: 99..109
IDENTIFICATION METHOD: E
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LOCATION: 31.35
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: -19..-1
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703)816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 139 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
FEATURE:
NAME/KEY: domain
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79.7%; Score 604; DB 1; Length 139;

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3: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
       CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YYGYMFAYWGQGTLVTVSA 139
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                                                        NAME/KEY: domain
LOCATION: 50.66
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 0
                                                                                                                                                                                                           LOCATION: 99.109
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Best Local Similarity 82.77
Matches 115; Conservative
     IDENTIFICATION METHOD:
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COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acic
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ADDRESSEE: NIXON & V
STREET: 1100 NORTH C
CITY: ARLINGTON
                                                                                                                                                        OTHER INFORMATION:
                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                        FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                         US-08-438-562-1
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                                                                                                                                   61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                        61 GKSLEWIGYIYPNNGGTGYNQKFKSKATLTVDKSSSTAYMELHSLTSEDSAVYYCATYGH 120
                                                                              Gaps
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                         ;
                       18; Indels
                                                        1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
82.7%; Pred. No. 3.2e-55;
                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WITH KNOWN SEQUES
ESTABLISHED CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08438562
Patent No. 5874255
                                                                                                                                                                                                                                            121 YYGYMFAYWGOGTLVTVSA 139
                                                                                                                                                                                                                                                                                                                                                                                                   NAKAMURA, KAZUYASU
                                                                                                                                                                                                                                                                                                                                                                                                                   KOIKE, MASAMICHI
SHITARA, KENYA
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amino acid
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LOCATION: -19...1
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
Best Local Similarity 82.7
Matches 115; Conservative
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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LOCATION: 31..35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: ARLINGTON
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61 GKILEWIGYIYPYNGVSDYNONFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GKSLEWIGYIYPNNGGTGYNQKFKSKATLTVDKSSSTAYMELHSLTSEDSAVYYCATYGH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGWSWIFLFLLSGTAGVLSEVOLOOSGPELVKPGASVKISCKASGYTFTDYNMDWVKOSH 60
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                                                                                                        BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches 18; Indels
/product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                         /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Ralease #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 534
TELECOMMAN: 534
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APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBU
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
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US-08-116-778E-3
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US-08-438-562-3
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
CONSENSUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
                                                                                                                                                                                                                    /product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                          /product= "HYPERVARIABLE REGION 2"
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                                                                              ESTABLISHED CONSENSUS
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APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/116,778E
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    CONSENSUS
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                                                                                                                   NAME/KEY: domain
LOCATION: 31..35
IDENTIFICATION METHOD: E
IDENTIFICATION METHOD: O
IDENTIFICATION METHOD: O
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LOCATION: 50.66
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 0
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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Best Local Similarity 82.7
Matches 115; Conservative
                                                         IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
FEATURE:
sig_peptide
                    LOCATION: -19...-I
IDENTIFICATION METHOD:
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  NAME/KEY:
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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LOCATION: 31.35
LOCATION: 31.35
LOCATION METHOD: BY SIMILARITY
LDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTAI
LDENTIFICATION METHOD: CONSENSUS
OFFHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FRATURE: Admain
LOCATION: 55.66
LDENTIFICATION METHOD: BY SIMILARITY
LDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTAI
LDENTIFICATION METHOD: CONSENSUS
LDENTIFICATION METHOD: CONSENSUS
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OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
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/product= "HYPERVARIABLE REGION 2"
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Patent No. 5874255;
GENERAL INPORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KENYA
APPLICANT: KUWANA, YOSHHISA
APPLICANT: KUWANA, YOSHHISA
APPLICANT: HASEGAWA, MAMORU
ITILB OF INVENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONSENSUS
                                                  ATTORNET TARENT TREATHER.

REGISTRATION NUMBER: 32,955
REGISTRATION NUMBER: 249-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: alinear
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ATTORNEY/AGENT INFORMATION:
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LOCATION: 99..107
IDENTIFICATION METHOD: B
IDENTIFICATION METHOD: VIDENTIFICATION METHOD: 0
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LOCATION: -19...1
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FEATURE:
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Matches 115; Conservative
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61 GKSLEWIGYIYPNNGGTGYNQKPKSKATLTVDKSSSTAYMELHSLTSEDSAVYYCAR--A 118
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IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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CONSENSUS
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WITH KNOWN SEQUENCE OR TO AN ESTABLISEHD
CONSENSUS
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NAME/KEY:
COCATION: 99-11070
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTIDANTIFICATION METHOD: CONSENSUS
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ZIP: 22201-4714

COUNTRY: U.S.A.

ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUW TYEE: CIPPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: O'-JUM-95
CLASSIFICATION: 197-900
TELECOMMUNICATION INFORMATION:
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APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                            Sequence 93, Application US/08483528B
Patent No. 5939532
                                                                                     121 GSGYYFDYWGQGTTLTVSS 139
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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CORRESPONDENCE ADDRESS:
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NAME/KEY: domain
LOCATION: 55..66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OD: BY SIMILARITY
OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
OD: CONSENSUS
//product= "HYPERVARIABLE REGION 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OD: BY SIMILARITY
OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
OD: CONSENSUS
/product= "HYPERVARIABLE REGION 2"
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OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISEHD
OD: CONSENSUS
/product= "HYPERVARIABLE REGION 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.3%; Score 586; DB 1; Length 137; 82.7%; Pred. No. 2.3e-53; ive 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISH PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
SOFFWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATYONEY/AGENT INFORMATION:
NAME: WILSON, MARY 32,955
REGISCHATION NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acids
                                                                        ADDRESSEE: NIXON & VANDER STREET: 1100 NORTH GLEBE CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: domain
LOCATION: 31.35
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 1
IDENTIFICATION METHOD: 0
OTHER INFORMATION: /prov
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LOCATION: -19...1
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
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LOCATION: 55..66
IDENTIFICATION METHOD: E
IDENTIFICATION METHOD: V
IDENTIFICATION METHOD: V
OTHER INFORMATION: /proc
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LOCATION: 99..107
IDENTIFICATION METHOD:
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Matches 115; Conservative
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                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                               STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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TOPOLOGY:
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                                                                                              1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                         1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMDWVKQSH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 158, Application US/09647468

Sequence 158, Application US/09647468

Patent No. 6677436

GENERAL INFORMATION:

APPLICANT: SATO, KOH

APPLICANT: YABUTA, NACHING

TITLE OF INVENTION: HUMBAIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) A

TITLE OF INVENTION: HUMBER: US/09/647,468

TITLE OF INVENTION NUMBER: US/09/647,468

CURRENT PELING DATE: 1999-04-02

PRIOR PILING DATE: 1999-04-02

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 158

LENGTH 137
                                                  Gaps
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OTHER INFORMATION: sequence coding for H chain V region of ant-TF;
OTHER INFORMATION: mouse monoclonal antibody ATR-8
                                                  .,
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Query Match
77.3%; Score 586; DB 1; Length 137;
Best Local Similarity 82.7%; Pred. No. 2.3e-53;
Matches 115; Conservative 5; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.9%; Score 568; DB 2; Best Local Similarity 75.4%; Pred. No. 1.7e-51; Matches 107; Conservative 11; Mismatches 16;
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Sequence 27, Application US/08137117D

Fatent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: ARON
APPLICANT: BRNDIG, Mary
APPLICANT: BUNDIG, Mary
APPLICANT: UONES, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GSGYYFD---YWGQGTTLTVSS 139
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ORGANISM: Mus sp.
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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Pred. No. 2.2e-51;
8; Mismatches 18; Indels
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Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BRNDIG, Mary
APPLICANT: SALOANS, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
                              RESHAPED HUMAN ANTIBODY TO HUMAN INTERLEUKIN-6 RECEPTOR
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: BALENTIN Release #1.0, Version #1.30
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 53466/126/AAOK
TELECOMMUNICATION NUMBER: 53466/126/AAOK
                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Weakington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 -GGNRFAYWGQGTLVTVSA 135
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Best Local Similarity 78.4%;
Matches 109; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TITLE OF INVENTION: RESTITLE OF INVENTION: INT.
NUMBER OF SEQUENCES: 156
CORRESPONDENCE ADDRESS:
STRRFF
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Search completed: March 20, 2006, 07:31:35 Job time : 8.40237 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSGIFLFLLSGTAGVHSEIQLQQSGPELMKPGASVKISCKASGYSFTSYYIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
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Pred. No. 2.2e-51;
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Sequence 4, Application PC/TUS9311612
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIPCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
RILING DATE: 24-APR-1992
RILING DATE: 24-APR-1992
RICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
RICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATOld C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFENCE/DOCKET NUMBER: 53466/126/AAOK
FELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                      3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 -GGNRFAYWGQGTLVTVSA 135
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                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.8%;
78.4%;
                                                                                                                                                                            COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INPORMATION FOR SEQ ID NO: SEQUENCE CHRACTERISTICS:
LENGTH: 135 ami-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.8
Best Local Similarity 78.4
Matches 109; Conservative
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                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEWSWIFLFLLSGTAGVHSEVQLQQSGPDLVKPGASVKMSCKASGYTFTSYVMHWVKQKP 60
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
GURRANT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 566.5; DB 4
Pred. No. 2.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
                                                                                                                                                                        FILING DATE:
CLASCIPICATION:
PRIOR APPLICATION NUMBER: US 07/983,946
PILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GSGY-YFDYWGQGTTLTVSS 139
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                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION
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77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.7%;
Best Local Similarity 77.1%;
Matches 108; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                           US-10-687-035-34
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1 MGMSWIFLFLLSGTAGVHSE......FGSGYYFDYWGQGTTLTVSS 139
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 100 summaries
                                                   protein search, using sw model
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AAX80293
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Match Length
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Perfect score:
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Score

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Searched:

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Novel chi SM5-1 chi Novel chi chSMVH/Fc

Thrombopo Mouse SM5 Novel chi

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The present invention describes an isolated antibody, or an antigenbinding antibody fragment (1), that preferentially binds cell-associated binding antibody fragment (1), that preferentially binds cell-associated CA 125/0772 polypeptide relative to shed CA 125/0772 polypeptide. Also described: (1) a monoclonal antibody that competes with binding of (11); (3) a hybridoma as deposited in (11); (4) an isolated nucleic acid molecule (111) comprising a nucleotide sequence that encodes a variable chain region of (1); (5) a pharmaceutical composition comprising an antibody or an antigen-binding antibody fragment that preferentially binds cell-associated CA 125/0772P polypeptide, and a carrier; (6) a pharmaceutical composition comprising on antibody or an antigen-binding monoclonal antibody or an antigen-binding monoclonal antibody fragment comprising an antibody, or an antigen-binding material and a composition of manufacture (1V) comprising packaging material and a composition comprising an antibody, or an antigen-binding antibody fragment that preferentially binds cell-associated CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P operably linked to a neterologous antibody fragment, which preferentially binds cell-associated CA 125/0772P relative to shed CA 125/0772P operably linked to a heterologous antibody fragment, which preferentially binds cell-associated CA 125/0772P-related CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative CA 125/0772P relative CA 125/0772
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Novel chi
chSMVH/Fc
Novel chi
                                                                                                                                                                                                                                                                                                                                                                                                                        cell-associated CA 125/0772P; monoclonal antibody; cytostatic; immunostimulant; mediator of lysis; tumour; cell proliferative disorder; cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                          Antibody 776.1 heavy chain variable region (776.1H) SEQ ID NO:34.
Adv98549 P
Adv92488 c
Adv98551 P
                                                                                                                                                                                                                                                                                                                                                                                                     antibody; antigen-binding antibody fragment;
                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 38; SEQ ID NO 34; 153pp; English
ADV98549
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ADV98551
                                                                                                                                                                                                                         ADS94335 standard; protein; 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2002; 2002US-0418828P.
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    71.271.271.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian cancer.
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antibody fragment; (11) an antibody or antigen binding antibody fragment that competes with (VI) and (12) a pharmacettical composition comprising (VI) and a carrier. (11) has cytostatic activity, and can be used as an immunostimulant and a mediator of lysis of positive tumour cell. (1) is useful for ameliorating a symptom of a Ch 125/O7P-related disorder which is a cell proliferative disorder such as cancer, cervical or uterine cancer, breast or lung cancer or ovarian cancer. (V) is useful diagnostically for monitoring the development or progression of cancer or tumour as part of clinical testing procedure. The present sequence represents an antibody heavy chain variable region amino acid sequence, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                              61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a variable region of the heavy chain of an anti-Fas antibody. The constant region of the heavy chain is derived from human immunoglobulin G (IgG). The anti-Fas antibody can be used for the treatment and diagnosis of autoimmune diseases
                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                      1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                   1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding, e.g. variable region of anti-Fas antibody - useful for, diagnosis and treatment of auto-immune diseases.
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variable region; heavy chain; anti-Fas antibody; human; mouse; immunoglobulin G; IgG; light chain; treatment; diagnosis; autoimmune disease.
                                                                                                                                                                                                                                                         100.0%; Score 758; DB 8; Length 139; 100.0%; Pred. No. 6.9e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variable region of an anti-Fas antibody heavy chain.
                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW60866 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 13; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GSGYYFDYWGQGTTLTVSS 139
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96JP-00268737.
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Best Local Similarity 100.
Matches 139; Conservative
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Sequence 135 AA;

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GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                    AAW31751;
                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                      RESULT 4
                                                                                                                                                         AAW31751
                               원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fas antigen, and controls and induces apoptosis in cells which expressed amino acids sequences obtained from a mammal other than human, other regions contain amino acid sequences from human and they partly contain modified amino acids sequences from human and they partly contain modified amino acids sequences from human and they partly contain modified amino acids. (A) has immunosuppressive activity. (A) is used for represents an immunoglobulin M chimeric antibody heavy chain variable region from an example from the present invention
                                                                                                                                        GKSLEWIGYIYPYNGGTGYNQKFKSKATLIVDNSSSTAYMELRSLTSEDSAVYYCAR--- 117
                                                                                                                      GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant antibody (A) which binds to
                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel recombinant antibody used for treating and diagnosing autoimmune diseases - is humanized anti-Fas antibody which controls and induces apoptosis in cells expressing fas antigen.
                                                                               1 MGWSWIFLELSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
diagnosis; CDR; complementarity determining region; apoptosis;
                                  4.
                                                                                                                                                                                                                                                                                                                                                                                    chimeric antibody heavy chain variable region SEQ ID NO:1.
    Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 135;
                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 644; DB 3;
Pred. No. 2.5e-46;
 Score 644; DB 2;
Pred. No. 2.5e-46;
                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 9-10; 25pp; Japanese.
                                                                                                                                                                                                                                                                                         AAY80293 standard; protein; 135 AA
                                                                                                                                                                                                                 -SYYAMDYWGQGTSVTVSS 135
                                                                                                                                                                                  121 GSGYYFDYWGQGTTLTVSS 139
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87.8%;
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                               Conservative
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Matches 122; Conservative
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               al Similarity
122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ95282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2000014383-A.
                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
Synthetic.
Query Match
Best Local S
Matches 122
                                                                                                                      61
                                                                                                                                                                                                                                                                                                                         AAY80293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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9 9

4,

8; Indels

5; Mismatches

MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH

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This sequence represents the heavy chain of the protein of the invention. The protein of the invention is a recombinant protein (A), that comprises at least one region corresponding to an immunoglobulin (Ig) variable region which enables the protein to recognises and specifically bind to an antigen, preferably human Fas, and has ubstantially no more immunogenicity in a human patient than a human antibody. The proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGMSWIFLFLEGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas; antibody; human; immunoglobulin; variable region; rheumatism; autoimmune disease; rheumatoid arthritis; therapy; CDR; heavy chain; complementarity determining region.
Anti-Fas recombinant antibodies - useful for treating auto-immune diseases, especially rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakahara K, Yonehara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.0%; Score 644; DB 2;
llarity 87.8%; Pred. No. 1.2e-45;
Conservative 5; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H chain subunit of Fas specific antibody

    19
    note= "signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 29-31; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                           Ŕ
                                                                                121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                       118 -SYYAMDYWGOGISVTVSS 135
                                                                                                                                                                                                                                                                                           AAW31751 standard; protein; 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-00302415.
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-482673/45.
N-PSDB; AAT88869.
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Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1997
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AAW71888 ID AAW RESULT

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The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a J segment, has apoptosis inducing activity, and does not include a J segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially. The IgM molecule used in the invention has bluman Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAA12202-A78272) and the Corresponding protein sequences (see AAA12303-B12918 and AAB12919), and cucleotide sequences of the humanised anti-human Fas Ig CH11 (see CAAA78202-A78206) and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12907). CC AAA78202-A78206 and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12907). CC Chains used in the invention are represented by sequences AAA78217-A78318 and AAA78335-CC A78337, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78314 and AAA78338-A78367. Primer sequences AAA78212 are specific for murine Ig DNA, and are used in the production of the agent of the invention
                                                                                                      61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                       Anti-human Fas humanizing antibody-containing antirheumatic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-human Fas antibody CH11 H chain protein sequence SEQ ID #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer; immunosuppression; autoimmune disease; treatment; rheumatism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 644; DB 3; Length 590;
Pred. No. 1.2e-45;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 47-48; 109pp; Japanese.
                                                                                                                                                                                                                                                                                                               AAB12908 standard; protein; 590 AA.
                                                                                                                                                                    121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                          98JP-00264598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.8%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-00263984
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-454476/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-Fas antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA78202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2000154149-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                        AAB12908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of the heavy chain of the mouse anti-human Fas monoclonal antibody CH11, as deduced from an amplified CDNA clone (see AAV66735). The invention relates to novel humanised antibodies comprising humanised light and heavy chains (see AAW71876-81) of CH11. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synovicotytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodies - for use in inducing treatment of auto:immune
      GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis; autoimmune disease; rheumatoid arthritis; therapy; human; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yonehara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 644; DB 2; Length 590;
Pred. No. 1.2e-45;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of anti-Fas protein humanised antibodies apoptosis on Fas expressing cells in the treatment o diseases, especially rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                            Anti-human Fas monoclonal antibody CH11 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 58-60; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 19
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mat_protein
                                                                                                                                                                                                                                       AAW71888 standard; protein; 590 AA
                                                                                         139
                                                                                                               -SYYAMDYWGQGTSVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.8%;
Matches 122; Conservative
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                                                                                         GSGYYFDYWGQGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50. .54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69. .84
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-00302113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118. .124
/label= CDR3
                                                                                                                                                                                                                                                                                                                    (first entry)
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/label= Ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haruyama
                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-482965/42.
N-PSDB; AAV66735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                      18-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serizawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP866131-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                         121
                                                                                                                                                                                                                                                                             AAW71888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
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Region Region Region

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Gaps

4

61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120

Gaps

4

Length 135; 10; Indels

Score 625; DB 2; Pred. No. 9.7e-45; 7; Mismatches 10

Query Match 82.5%; Best Local Similarity 84.9%; Matches 118; Conservative

Query Match Best Local Similarity Sequence 135 AA;

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This is the amino acid sequence of the heavy chain of the M195 anti-CD33 antibody. This antibody selectively binds to surface of haematopoeitic progenitor cells (HPC) and is transported into the cells by endocytosis. The invention provides conjugates of human Fanconi anaemia complementation group C (FAC) protein (see AAW68546) and anti-CD33 antibody (preferably a single chain antibody). A nucleic acid (see AAW33947) encoding the heavy chain can be ligated with vector pED6 and with FAC cDNA (see AAW33945) to provide a fusion protein. Alternatively, nucleic acids encoding the heavy and light chains (see AAW68549) of M195 are ligated into a bicistronic vector, antibody molecule is isolated from transfected cells, and chemically crosslinked to FAC protein (see AAW68946) to form a conjugate. The conjugate or fusion protein, or a nucleic acid encoding it, can be used to deliver FAC to an HPC, specifically to inhibit apportosis, particularly in patients exposed to high doses of chemotherapy for treatment of non-myeloid cancers, also to treat Panconi anaemia (by complementation of the genetic defect).

Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant production of conjugate in cell cultures) or in vivo. Treatment with FAC may eliminate the need for extensive bone marrow transplants to reserve the analycopolesis after chemotherapy. (Updated on 27-NUG-2003 to correct OS
                                                                          GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                            GKSLEWIGYIYPYNGGTGYNQKFKSKATLTVDNSSSTAYMELRSLTSEDSAVYYCAR--- 117
  9
                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panconi anaemia complementation group C; PAC; apoptosis; haematopoiesis;
bone marrow; chemotherapy; gene therapy; CD33; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New conjugate of Fanconi anaemia molecule and peptide selective for haematopoietic precursor cells - inhibits apoptosis of these cells, for treating Fanconi anaemia and patients undergoing high-dose chemotherapy
                      1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH
MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 50-51; 72pp; English.
                                                                                                                                                                                                                                                                                      AAW68548 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                          -SYYAMDYWGQGTSVTVSS 135
                                                                                                                                                  121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-CD33 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0046546P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US009975
                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
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N-PSDB; AAV33947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Youssoufian H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9851792-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1998;
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15-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                            AAW68548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia.
                                                                                                            61
                                                                                                                                                                                          118
                                                                          61
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The present invention describes a method of producing humanised coding a humanised involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-thost disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CWV virus infections and myeloid
                                                                                                                                                                                                                                                                                          Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Producing humanized immunoglobulin, involves producing a cell containin
DNA segments encoding humanized heavy and light chain variable regions,
and expressing the DNA segments in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia. The present sequence is an antibody used to demonstrate nethod of the invention
                                                                                                                                                                                                                                                           Murine M195 antibody heavy chain SEQ ID NO: 69.
                                                                                                                                                           AAB69682 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Pig 34; 145pp; English.
                                               121 GSGYYFDYWGQGTTLTVSS 139
                                                                ||||||::||||
118 -GRPAMDYWGQGTSVTVSS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00290975.
89US-00310252.
90US-00590274.
90US-00634278.
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                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Queen CL, Selick HE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-190856/19.
N-PSDB; AAF58738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           US6180370-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                             30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-FEB-1989;
28-SEP-1990;
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Vanwezenb PM,
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Designing humanized immunoglobulin chain comprises substituting human framework amino acids of acceptor immunoglobulin with corresponding amino acid from donor immunoglobulin at position in immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Ig) chain. The method comprises substituting human framework amino acids of the acceptor Ig with a corresponding amino acid from the donor Ig at a position in the Igs, where the amino acid is immediately adjacent to one of the CDR's or the amino acid is predicted to have a side chain atom whose Van der Waals surface is 3 angstroms from the CDR's in threedimensional Ig model and is capable of interacting with the antigen or
                                                                                                    GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                     1 MGWSWIFLFFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of designing a humanised immunoglobulin
                                                                                                                                                                                                                                                                                    humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig; donor Ig; CDR; complementarity determining region; interleukin-2; IL-2; IL-2 receptor; T-cell mediated disorder; mouse; M195 antibody; heavy chain variable region.
                                                  MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coelingh KL;
          Length 135;
                            10; Indels
                                                                                                                                                                                                                                                                   Mouse M195 antibody heavy chain variable region #2.
         Score 625; DB 4;
Pred. No. 9.7e-45;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Landolfi NF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 41; 130pp; English.
                                                                                                                                                                                                        ADO47773 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schneider WP,
                                                                                                                                 121 GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                            -GRPAMDYWGQGTSVTVSS 135
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89US-00310252.
90US-00590274.
95US-00484537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995; 95US-00484537
22-NOV-2000; 2000US-00718993
          82.5%;
84.9%;
                                                                                                                                                                                                                                               (first entry)
        Query Match
Best Local Similarity 84.9
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LANDOLFI N F. COELINGH K L. SELICK H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHNEIDER W P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-304235/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QUEEN C L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Co MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADO47772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CO M S.
                                                                                                                                                                                                                                               15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Queen CL,
Selick HE;
                                                                                                                                                                                                                            ADO47773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (QUEE/)
(COMS/)
(SCHN/)
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                                                                                                                                                                                                                                                                                                                                         Mus sp.
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cc with the CDR's of the humanised Ig that when the chain is a heavy chain, substituted amino acid(s) is capable of interacting with CDR's 2 or 3.

Also described are: an Ig comprising two light/heavy chains; a DNA sequence which upon expression encodes a humanised Ig chain; a composition comprising a bNA sequence coding for a humanised Ig; a composition comprising a pure humanised immunoglobulin capable of inhibiting binding of human interlewin-2 (IL-2) to a human IL-2 receptor; treating T-cell mediated disorders in a human patient comprising administering to the patient a therapeutic dose of an Ig; and a composition comprising a pure humanised Ig reactive with the p75 chain of the human IL-2 receptor. The method is used for designing a humanised immunoglobulin chain, useful for treating T-cell mediated disorders in a human patient. The invented method produces an Ig chain that is easily can deconomically produced. This is the amino acid sequence of mouse M195 antibody heavy chain variable region. Residues in the human antibody to create in humanised antibody.

C a humanised antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavy chain variable domain of human chorion gonadotrophin-binding pptde.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human chorionic gonadotropin; antibodies; heavy chain; choriocarcinoma; abortion; tumour detection; complementary determiming regions;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGMSWIFLFLEGTAGVASEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.5%; Score 625; DB 8; L
84.9%; Pred. No. 9.7e-45;
ive 7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GSGYYFDYWGQGTTLTVSS 139
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/label= CDR 2
118. .126
/label= CDR 3
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/label= CDR 1
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(first entry)
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Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-site
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04-OCT-1990
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'note=
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                                                                                                                                                                             Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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 useful for
mutans and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabbit; immunoglobulin; receptor; protection protein; mutans; heavy chain; antigen binding domain; protection; pathogen; mucosal; environment; gastrointestinal; passive; immunisation; Guy's 13 antibody; prevention; dental caries; Streptococcus; poly; gamma chain.
                                                                                                                   forms a hCH-binding antibody fragment (FhCG). For the production of Abs the variable region was fused to a constant region of human origin. The product can be used to prevent pregnancy or for combatting choriocarcinomas or other hCG-producing tumours. They also have diagnostic applications as immune reagents for in vivo diagnosis, eg for localisation of tumours and for in vivo diagnosis for detection of hCG in body fluids. (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin and protection protein complex and its prodn. in plants
                                                                                                                                                                                                                                                                                         1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMIWVKQSH
                                                                                                                                                                                                                                                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                        Togheter with the light chain variable domain (AAR05089) the sequence
                                         Polypeptide(s) which specifically bind human chorionic gonadotropin contg. antigen-binding domains comprising complementary determining regions.
                                                                                                                                                                                                                               Query Match 82.2%; Score 623; DB 2; Length 137; Best Local Similarity 84.2%; Pred. No. 1.5e-44; Matches 117; Conservative 9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guy's 13 anti-Streptococcus mutans antibody gamma chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLANET BIOTECHNOLOGY INC.
UNITED MEDICAL & DENTAL SCHOOLS GUYS.
                                                                                     -pp; English
                                                                                                                                                                                                                                                                                                                                                                             119 GIFYTMDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                   GSGYYFDYWGQGTTLTVSS 139
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95US-00434000
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                                                                                     Disclosure; Page ?;
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                    N-PSDB; AAQ04694
                                                                                                                                                                                                           Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT31293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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04-MAY-1995;
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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   mucosal antigens, esp. against S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEWIWVFLFLLSGTAGVHSGVOLOOSGPDLVKPGASVKISCKASGYTFTDYNIHWVKOSR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody, Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750; KM-603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 613.5; DB 2;
Pred. No. 8.8e-44;
6; Mismatches 10;
passive immunisation against mucosal S. sorbinus to prevent dental caries
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/label= sig_peptide
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                                                                                             Claim 23; Page 131; 152pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR53328 standard; protein; 139
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/label= CDR1
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Best Local Similarity 83.5%;
Matches 116; Conservative
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/label= (
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(first entry)
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Best Local Similarity 82.77
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                  Nakamura K, Hanai N,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-468416/39.
N-PSDB; AAX99474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 139 AA;
                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                                                                                                                                    07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1999
                                                                                                                          US5939532-A
                                                                                                                                                                   17-AUG-1999
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                                                                                                                                                                                                                                             Chimeric human Ab expression vectors are constructed by inserting the Ab heavy and light chain variable region-encoding CDNA isolated from the hybridomas producing a mouse or rat monoclonal Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy and light chain constant region-condition CDNA. The expression vectors are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be comperior to mouse monoclonal Abs in the efficacy in the treatment of human cancer, for instance. Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603 heavy and light chain sequences are given in AAQ45426-CDR regions for use in chimeric Abs are indicated in the Features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSWIFLFLESGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMDWVKQSH 60
                                                                                                                                               Humanised antibody specific for ganglioside GM2 - used for producing a cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                         Hasegawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; nucleotide; genomic; hypervariable region; chimeric;
light chain; heavy chain; amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.7%; Score 604; DB 2; Length 139; 82.7%; Pred. No. 5.8e-43; ive 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody chain used to produce Human chimeric antibodies.
                                       Kuwana Y,
                                         Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .19
'label= Signal peptide
                                                                                                                                                                                                               Claim 5; Page 104-105; 191pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28356 standard; protein; 139 AA
                                         Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KYOW ) KYOWA HAKKO KOGYO KK.
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(first entry)
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                                         Koike M,
                                                                                  WPI; 1994-126857/16.
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                                                                                                        N-PSDB; AAQ45426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 139 AA;
                                           Nakamura K,
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04-NOV-1999
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMDWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kuwana Y, Hasegawa M, Koike M, Shitara K;
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light chain; heavy chain; plasmid; hypervariable.
                                                      /18. 129
/label= CDR3
/note= "Complementarity determining region"
/label= CDR2
/note= "Complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.7%; Score 604; DB 2; Length 139; 82.7%; Pred. No. 5.8e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-GM2 heavy chain from KM796 mouse hybridoma cell line.
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    19

            11 . 19
            12 . 139
            13 Mature mouse heavy chain

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric human antibody expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 81-83; 188pp; English.
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                                                                                                                                                                                                                                                                                                             95US-00483528.
                                                                                                                                                                                                                                                                                                                                                                       93US-00116778.
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This amino acid sequence was isolated from mouse hybridoma cell line KM-796, and encodes for the anti-GM2 heavy chain. Chimeric human antibodies of the invention are useful in the treatment of cancer, especially that which is of neural ectodermal origin. In contrast to prior art constructs based on mouse monoclonal antibodies, the chimeric human antibodies do antibodies anti-mouse immunoglobulin production. The chimeric human antibodies antibodies have a prolonged half-life and a reduced frequency of adverse effects when compared to mouse monoclonal antibodies
                                                                                                                                                                                                                                          Shitara K;
                                                                                                                                                                                                                                          Koike M,
                            69. .85
/label= Hypervariable region 2
                                                         118. .128
/label= Hypervariable region 3
                                                                                                                                                                                                                                          Наведама М,
                                                                                                                                                                                                                                                                                               Chimeric human antibody expression vectors.
                                                                                                                                                                                                                                                                                                                           Example 1; Col 151-153; 188pp; English.

    .54
    label= Hypervariable

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                                                                                                                                                      95US-00483528
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                                                                                                                                                                                                             HAKKO KOGYO
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                                                                                                                                                                                                                                                                     WPI; 1999-468416/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 139 AA;
                                                                                                                                                                                                             (KYOW ) KYOWA
                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                  07-SEP-1993;
                                                                                               US5939532-A.
                                                                                                                                                                                                                                         Nakamura K,
                                                                                                                          17-AUG-1999.
 Domain
                            Domain
                                                        Domain
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GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                             GKSLEWIGYIYPNNGGTGYNOKFKSKATLTVDKSSSTAYMELHSLTSEDSAVYYCATYGH 120
                                                                                               9
                                                                                             1 MGWSWIFLFLLSGTAGVLSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMDWVKQSH
                                   ö
    Length 139;
                                   18; Indels
   Score 604; DB 2;
Pred. No. 5.8e-43;
6; Mismatches 18;
                                                                                                                                                                                                            || | |||||| :||||:
121 YYGYMFAYWGQGTLVTVSA 139
                                                                                                                                                                                          121 GSGYYFDYWGQGTTLTVSS 139
 79.7%;
82.7%;
Query Match
Best Local Similarity 82.7
Matches 115; Conservative
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Human penton base monoclonal antibody, DAV-1 heavy chain fragment.
     AAE18372 standard; protein; 438 AA
                                (first entry)
                                07-MAY-2002
                   AAE18372;
AAE18372
       2444444444444444
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Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer; wascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder; hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain; cytostatic; vasotropic; ophthalmological.

Mouse; bifunctional molecule, antigen-binding portion, alpha integrin, cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;

Portion of mouse DAV-1 heavy chain monoclonal antibody

(first entry)

10-MAY-2003

ABG76347;

ABG76347 standard; protein; 438 AA

ABG76347

signalling pathway; targeted gene therapy; delivery vector; adenoviral gene delivery particle; viral infection; cancer; rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder; hyperproliferative disorder; hormonal disorder; virucide; antiinflammatory; antirheumatic;

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WO200204522-A2
Homo sapiens
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17-JAN-2002

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antibody or its antigen-binding portion, and a targetting agent where the antibody specifically binds to an antigen in a protein that binds to avintegrin, and the targetting agent specifically binds to a cell surface protein that activates the phosphatidylinositol 3 (PISK) signalling pathway. The bifunctional molecules are useful for gene therapy, for promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking av integrins, for enhancing Ad binding and internalisation, and in gene delivery of by fibreless adenovirus particles. The bifunctional molecules permit targetting of viral and bacterial vectors to cells that express targetted receptors. Diseases that can be targetted include cancers, vascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence is human penton base monoclonal antibody, DAV-1 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GKSLEWIGYIYPYKGCTGYNQKFKSKATLTTDSSSNTAYMELRSLTSDASAVYYCARG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH 60
                                                                                                                                                                                                                                                                                                   or its antigen-binding
                                                                                                                                                                                                                                                                                                                       portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av
                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to a bifunctional molecule comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGWSWIPLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                              New bifunctional molecules comprising an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.2%; Score 600.5; DB 5; 82.0%; Pred. No. 3.9e-42; ive 6; Mismatches 12;
                                                                                                   (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERPINDUNGEN VERW GES MBH.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10; Page 96; 106pp; English
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                  09-JUL-2001; 2001WO-EP007878.
                                                          10-JUL-2000; 2000US-00613017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 82.0
es 114; Conservative
                                                                                                                                                                                                                                 WPI; 2002-171707/22.
                                                                                                                                                                                                                                                      N-PSDB; AAE18372
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Li B;
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                                                                                                     WO200204522-A2
                                 Homo sapiens
                                                                                                                                                                                                                                               Nemerow GR,
                                                                                                                            17-JAN-2002
                                                                                                                                                                                                                                                                                                                                              integrins
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                                                        Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents a portion of the mouse DAV-1 heavy chain that is used for a fusion protein bifunctional antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer; vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                               New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGMSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human penton base monoclonal antibody, DAV-1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
antiarthritic; ophthalmological; DAV-1 heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 600.5; DB 5;
Pred. No. 3.9e-42;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                          Claim 10; Page 35-36; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE18370 standard; protein; 456 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IAYWGOGTLVTVSA 132
            penton base monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%;
82.0%;
                                                                                                                             10-JUL-2000; 2000US-00613017.
                                                                                                       10-JUL-2001; 2001US-00903327.
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Best Local Similarity 82.0
Matches 114; Conservative
                                                                                                                                                                (SCRI ) SCRIPPS RES INST.
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                                                                                                                                                                                                                          N-PSDB; ABX12746.
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                                                          US2002164333-A1
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AAE1837
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The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targetting agent where the antibody specifically binds to an antigen in a protein that binds to av integrin, and the targetting agent specifically binds to a cell surface protein that activates the phosphatidylinositol 3 (FIXK) signalling pathway. The bifunctional molecules are useful for gene therapy, for promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking av integrins, for enhancing Ad binding and internalisation, and in gene delivery of by fibreless adenovirus particles. The bifunctional molecules permit targetting of viral and bacterial vectors to cells that express targetted receptors. Diseases that can be targetted include cancers, vascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence is human penton base monoclonal antibody, DAV-1 heavy
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hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain; cytostatic; vasotropic; ophthalmological.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                /note= "Hinge region"
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                                                                                                                                                                                                       Location/Qualifiers
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----IAYWGQGTLVTVSA 132
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Mouse; bifunctional molecule; antigen-binding portion; alpha integriz cell surface protein; phosphatidylinositol-3-OH kinase; P13K; asignalling pathway; targeted gene therapy; delivery vector; alenoviral gene delivery particle; viral infection; cancer; rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder; hormonal disorder; virucide; antiinflammatory; antirheumatic; antiarthritic; ophthalmological; DAV-1 heavy chain;
                            Mouse DAV-1 heavy chain monoclonal antibody.
                                                                                                                           penton base monoclonal antibody
                                                                                                                                                                                                                         2000US-00613017.
2000US-0325781P.
                                                                                                                                                                                                      10-JUL-2001; 2001US-00903327
                                                                                                                                                                                                                                                       (SCRI ) SCRIPPS RES INST
          (first
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                                                                                                                                                                 US2002164333-A1
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          10-MAY-2003
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The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to a purished, specifically binds to a call by a integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (FIX) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid atthitis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents mouse DAV-1 heavy chain, penton base New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av Claim 10; Page 30-31; 49pp; English

Sequence 456 AA;

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GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
                                                                                                                                          င္မ
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                                                                              MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH
                                                            1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
                              7;
79.2%; Score 600.5; DB 5; Length 456; 82.0%; Pred. No. 4.1e-42;
                              Indels
                              12;
               Pred. No. 4.1e
6; Mismatches
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----IAYWGQGTLVTVSA 132
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                              Matches 114; Conservative
               Best Local Similarity
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ocular disease; hyperproliferation; hormone metabolism disorder; cytostatic; vasotropic; antidiabetic; ophthalmological; metabolic-gen.; DAV-1; heavy chain; antibody.
                                                                                                                                                                                                                    wew modified knob, useful for treating cancer, vascular disorders, diabetic retinopathies, restenosis and vascular, ophthalmic, hyperproliferative o hormonal disorders.
             AEB96754 standard; protein; 456
                                                                                                                                                  29-DEC-2004; 2004WO-IB004324.
                                                                                                                                                                09-JAN-2004; 2004US-0535199P
                                                      DAV-1 antibody heavy chain.
                                         (first entry)
                                                                                                                                                                              (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                          WPI; 2005-555928/56.
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                                                                                                                     WO2005075506-A1
                                        20-OCT-2005
                                                                                                                                    18-AUG-2005
                                                                                                                                                                                            Vemerow GR,
                                                                                                        Synthetic.
                           AEB96754;
RESULT 19
       AEB96754
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time invention relates to a modified adenovirus fiber protein comprising a fiber shaft that contains a sufficient number of shaft repeats to permit continuation in the absence of a fiber knob or in the absence of an extrinsic trimerization domain, and optionally a modified knob, where, if the knob is included, it is modified to remove or disable the continuation domain of the knob. The invention also relates to a modification of the knob removes or disables a trimerization domain of the knob removes or disables a trimerization domain of the knob, and the modified fiber protein comprising a sequence of nucleotides that encodes the modified adenovirus comprising the modified fiber, a composition formulated for comprising the modified fiber, a composition formulated for denoviral particle, where the binding of the particle to a native comprising the unmodified fiber, introducing the adenoviral particle, where the binding of the particle to a native containing the unmodified fiber, introducing the adenoviral particle into cells, introducing the cells into a subject and administrating the colls into a subject and administrating the colls into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administrating the cells into a subject and administration to the subject. The modified subject and administration and hormonal contents in a sequence represents a DAV-1 antibody heavy chain used in

Example 1; SEQ ID NO 28; 250pp; English.

Length 456; Indels 79.2%; Score 600.5; DB 9; 82.0%; Pred. No. 4.1e-42; ive 6; Mismatches 12; Best Local Similarity 82.0 Matches 114; Conservative Sequence 456 AA;

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61 GKILLEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120

Gaps

7 ;

Length 493; Indels

Sequence 493 AA;

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Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer; vascular disorder; disorder; catinopathy; restencesis; ophthalmic disorder; hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain; cytosteatic; vasotropic; ophthalmological; epidermal growth factor; EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av

    .439
/note= "N-terminal portion of DAV-1 heavy chain"

                                                                                                                                                                    Human N-terminal DAV-1 heavy chain-mature EGF fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERPINDUNGEN VERW GES MBH.
(SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                           441. .493
/note= "Human mature EGF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 101-102; 106pp; English.
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                        AAE18379 standard; protein; 493 AA
                                             |||||| :||||:
----IAYWGQGTLVTVSA 132
                                121 GSGYYFDYWGQGTTLTVSS 139
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                                                                                                                                                (first entry)
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Chimeric.
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61 GKILEWIGYIYPYNGVSDYNQNFKSKATLIVDNSSNTAYMELRSLTSEDSAVYYCARWDF 120
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                                                                                                                   1 MGWSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSH
   DB 5;
Score 600.5; DB 5
Pred. No. 4.5e-42;
6; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: March 20, 2006, 07:35:44
he : 54.3087 secs
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----IAYWGQGTLVTVSA 132
   79.2%;
                              Local Similarity 82.0
Les 114; Conservative
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      Query Match
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Matches
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

March 20, 2006, 07:28:38 ; Search time 23.7968 Seconds (without alignments) 3765.293 Million cell updates/sec Run on:

Sequence:

US-10-687-035-33 656 1 MDPQVQIFSFLLISASVIMS......YCQQWSSNPFTFGSGTKLBI 127 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q5xfy8 mus musculu	Q58ev6 mus musculu	Q8vdd0 mus musculu	Q811c3 mus musculu	Q569y8 mus musculu	P01680 mus musculu	Q8k1f3 mus musculu	P04940 mus musculu	Q8k1f2 mus musculu	P04943 mus musculu	P04942 mus musculu	mus	Q8k1f0 mus musculu	BUM	P04941 mus musculu	Q9j176 mus musculu	mus		mus		mus	P01677 mus musculu	P01679 mus musculu	Q9ul78 homo sapien	homo	P18135 homo sapien	Q52164 mus musculu	Q9j178 mus musculu	Q7z3y4 homo sapien	• • •	P01620 homo sapien
SUMMAKIES		a	QSXFY8 MOUSE	Q58EV6 MOUSE	Q8VDD0 MOUSE	Q811C3_MOUSE	Q569Y8_MOUSE	KV4A MOUSE	Q8K1F3_MOUSE	KV6F_MOUSE	Q8K1F2 MOUSE	KV61 MOUSE	KV6H_MOUSE	KV6J_MOUSE	Q8K1F0_MOUSE	Q9U410_MOUSE	KV6G_MOUSE	Q9JL76_MOUSE	KV6K_MOUSE	Q8K1F1_MOUSE	KV6B_MOUSE	KV6A_MOUSE	KV6D_MOUSE	KV6C_MOUSE	KV6E_MOUSE	Q9UL78_HUMAN	KV3M HUMAN	KV3L_HUMAN	O52L64 MOUSE	Q9JL78_MOUSE	Q7Z3Y4_HUMAN	Q7SZ36_XENLA	KV3B_HUMAN
át		B	~	~	7	~	N	Н	~	П	~		Н	Н	~	7	-	7	Н	~	Н	Н	Н	Н	-	~	-	Н	8	~	7	~	7
		Match Length DB	235	235	134	131	237	129	112	107	112	107	107	107	112	106	107	97	108	114	107	101	107	101	101	109	129	129	240	101	236	237	109
	Query	Match	87.5	81.2	80.2	78.0	72.1	68.9	66.2	65.4	65.2	64.6	64.5	64.5	64.3	64.2	64.0	63.9	62.3	62.2	60.2	59.8	59.6	59.5	57.2	53.4	53.2	53.0	52.7	52.1	52.1	51.6	51.5
		Score	574	533	526	511.5	473	452	434	429	428	424	423	423	422	421	420	419.5	409	408	395	392	391	390	375	350	349	348	345.5	341.5	341.5	338.5	338
	Result	No.	-	~	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

ALIGNMENTS

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121 AGTRLEL 127
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straueberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

REDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straueberg R.L., Zeeberg B.A., Grouse L.H., Derge J.G.,

Ralachenko L., Marusina R.S., Wagner L., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Depkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A ltschul S.F., Sarese M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Monton and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Director MGC Project;
Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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89.0%; Pred. No. 4.4e-47;
ive 3; Mismatches 11;
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InterPro; IPR003159; Ig.
InterPro; IPR007110; Ig.-11ke.
InterPro; IPR003597; Ig.-11ke.
InterPro; IPR003006; Ig.-11ke.
InterPro; IPR003596; Ig.-12ke.
InterPro; IPR003596; Ig.-12ke.
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SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50335; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SMR; QSXFY8; 23-235.
                                                                                                      PRT;
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Mus musculus (Mouse).

Eukarore. ween
                                                                                            QSXFY8_MOUSE PRELIMINARY;
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RY STEALNETURE SUCLENCE.

RY STEALURIE STREECOLON;

RY STEALURIE STREECOLON;

RY STRAINSTURE STREECOLON;

RA STRAINSTURE ST., Feingold E.A., Grouse L.H., Derge J.G.,

RIGHINE S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,

RIGHING S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.R., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rudding L., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Gennerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Gennerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodrights A. Schein J.E., Jones S.J.M., Marra M.A.;

R. Rodrights A. Schein J.E., Jones L.D., Dickson M.C.,

R. R. Rodrights A. Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.2%; Score 533; DB 2; Length 235; Best Local Similarity 81.9%; Pred. No. 3.9e-43; Matches 104; Conservative 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC091738; AAH91738.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGY; 1.
PROSITE; PSS0835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 235 AA; Z5719 MW; BE4E4ABDD2578252 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                    Last annotation update)
                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMR; OSBEWG; 23-235.

GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig. C1.
InterPro; IPR003597; Ig. C1.
InterPro; IPR003596; Ig. MHC.
InterPro; IPR003596; Ig. WHC.
InterPro; IPR003596; Ig. WHC.
Pfam; PF07654; C1-8et; 1.
SWART; SW00400; IGG; 1.
    PRT;
                                                                                    Created)
                                                                           10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FVB/N; TISSUE=Colon;
NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences."
QSBEV6_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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59 QKPGSSPKPWIYGTSTLASGVPTRFSGSGGTSYSLTISRVEAEDAATYYCQQWSSNP-F 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 QKPGSSPKLWIYSTSNLASGVPVRFSGSGSGTSYSLTISSVBAEDAATYYCQQYDSSPSI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDSQVQIFSFLLISALVIMSRGQIVLTQSPAIMSASPGEKVTWTCRASSSVRSSYLHWYQ 60
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                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin gamma-3 kappa chain.
                                                                                                                                                                                                                                                                                                  STRAIN=MRL/MpJ-lpr/lpr; TISSUB=Spleen;
MEDLINE=93156722; PubMed=8429833; DOT=10.1016/0161-5890(93)9008
Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.
"Cloning and cDNA sequence analysis of nephritogenic monoclonal antibodies derived from an MRL/lpr lupus mouse.";
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                                 )1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
)1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
|munoglobulin gamma-3 kappa chain precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
14083 MW; 5E83656954666E9E CRC64;
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Last annotation update)
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Pred. No. 2.4e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
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EMBL; D14629; BAA03482.1; -; mRNA.
HSSP; P01679; 2FBJ.
SMR; Q811C3; 23-131.
Ensembl; ENSWUSGO0000058987; Mus m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like
InterPro; IPR003596; Ig_v.
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Best Local Similarity 81.5%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q569Y8 MOUSE PRELIMINARY;
Q569Y8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 TFGSGTKLEI 127
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>131
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                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
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Best Local Similarity
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Name=Igk-C;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
     DTT DDT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT BD DTT B
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caton A.J., Brownlee G.G., Staudt L.M., Gerhard W.; "Structural and functional implications of a restricted antibody response to a defined antigenic region on the influenza virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                      01-MAR.2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-MGC 212 variable light chain (Fragment)
Name-Gm1502; Synonyms-anti-MGG kappa;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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Pred. No. 1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; PO1834;
SMR; Q8VDD0; 233-134.
SMR; Q8VDD0; 233-134.
Ensembl; ENSWUSGO000062047; Mus musculus.
MGI; MGI:2686348; Gm1502.
InterPro; IPR007110; Ig-like.
InterPro; IPR0071556; Ig-v.
SMART; SM00406; IGv; 1.
R PROSTTE; PS50835; IG LIKE; 1.
134 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O J. 5:1577-1587 (1986).
L; AJ416331; CAC94866.1; -; mRNA.
; G27887; G27887.
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                                                                                                                                                                                                                                         QBVDDO_MOUSE PRELIMINARY;
QBVDDO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QB11C3 MOUSE PRELIMINARY;
Q811C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chernajovsky Y.;
Submitted (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sembi P.;
Submitted (JAN-2002)
                                                  SGTKLEI 127
                                                                                    SIIIIS
AGTKLDL 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c;
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61
                                                     121
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Q811C3 MOUSE
ID Q811C3 MC
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14; Indels

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FGSGTKLEI 127
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129
129 AA;
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PubMed=2499887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=82115300; PubMed=6799208; DOI=10.1016/0092-8674(81)90033-7; Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.; Kwan S.-P., Max E.E., Seidman J.G., Leder P., Scharff M.D.; Two Samunoglobulin genes are expressed in the myeloma S107."; Cell 26:57-66(1981).

-I- MISCELLANEOUS: This protein, in which there is a deletion of two amino acids at the V-J recombination site (after position 118), is synthesized but not secreted in cells that express and secrete the normal kappa chain S107.
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodecgren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Kazywinski M.T., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
110-MAY-2005 (Rel. 47) Last annotation update)
Mus musculus (Mouse).

Bukarryota, Meazaos, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSV--IYMCWNQ
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                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SEQUENCE 237 AA; Z5978 MW; A88596AA47FFB932 CRC64;
                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 72.1%; Score 473; DB 2; Local Similarity 71.3%; Pred. No. 2.3e-37; neg 92; Conservative 15; Mismatches 20;
                                                                                                                                                                                                                                        EMBL; BC092251; AAH92251.1; -; mRNA. SMR; Q569YB; 23-237.
                                                                                                                                                                                                                                                                   InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PP07554; Cl-set; I.
SMART; SM004007; IGC1; I.
SMART; SM004007; IGC1; I.
                                                                                                                                                                                                    STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                 and mouse cDNA sequences.
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121 FGGTRLEL 129
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P01680;
                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSV--IYMCWNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V-IV region S107B. Framework-1. Complementarity-determining-1.
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STRANTB-RALBA, C: TISSUE-Hyperimmunized spleen;
STRON Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S. "Two murine natural polyreactive autoantibodies are encoded nonmutated germ-line genes."; B6:4624-4628(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PR05ITE; PS50355; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin V region; Signal.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
                                                                                                                                                                                                                                     PIR; A01943; KVMS7B.
HSSP; POL6679; ZBBJ.
SMS: POL660; 23-129.
Ensembl; ENSMUSGO0000059773; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-3.
                                                                                                                                                                               EMBL; J00577; AAA38780.1; -; Genomic_DNA
EMBL; V00780; CAA24157.1; -; Genomic_DNA
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Q8K1F3;
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NCBI_TaxID=10090;
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Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to
phenyloxazolone and its early diversification.";
                                                            MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761; Tillman D.M., Jou N.T., Hill R.J., Marion T.N.; Marion T.N.; Both IgM and IgG anti-DNA antibodies are the products of clc selective B cell stimulation in (NZB x NZW)F1 mice."; J. Exp. Med. 176:761-779(1992). EMBL, AFS16282; AAM64200.1; -; Genomic_DNA. PIR, A33933, A33933. PIR, PH1085; PH1085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 112;
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PROSITE; PS50835; IG LIKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 SGSGSGTSYSLTISRVEAEDAATYYCOOWSSNPFTFGSGTKLEI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;
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-!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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Pred. No. 6e-34;
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13-AUG-1987 (Rel. 05, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 Kappa chain V-VI region NQ2-17.4.1.
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                           Ensembl; ENSMUSG0000063156; Mus musculus.
InterPro; IPR00710; 19-11ke.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
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Ensembl; ENSMUSG0000062047; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
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HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.2%;
80.8%;
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SEQUENCE
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REGION
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23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR 82
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Сарв
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                                                                                                                                                                                                     Score 429; DB 1; Length 107; Pred. No. 1.7e-33; 9; Mismatches 14; Indele
                                                                Complementarity-determining-3. Pramework-4.
                       Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                     83 FSGSGSGTSYSLTISRVEAEDAATYYCOOWSSNPFTFGSGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                               84 SGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKLEI 127
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                                                                                                                                                          6F694284ECFA68E6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Anti-VIPase light chain variable region (Fragment).
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                                                                                                               By similarity,
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                                                 Framework-3
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01-OCT-2002 (TrEMBLrel. 22, Last seq
                                                                                                                                                        11561 MW;
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ilarity 78.1%;
Conservative
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Best Local Similarity
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P04943;

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                          This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroldea; Muridae; Murinae; Mus.
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                                 Length 107;
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Complementarity-determining-1.
Framework-2
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Complementarity-determining-3
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Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
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77.1%; Pred. No. 6.5e-33;
tive 9; Mismatches 15;
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                                                                                                                                                                                                                                                                                               Ensembl; ENSMUSG0000062047; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Framework-4
                                                                                                                                                                                                                                                  EMBL; K00739; AAA38684.1; -; mRNA.
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SMR; P04942; 1-107.
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NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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NUCLEOTIDE SEQUENCE.

REALINES 3271467; PubMed=6877353;

Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

Kaartinen Griffiths G.M., Markham A.F., Milstein C.;

Rattinen M., Griffiths G.M., Markham A.F., Milstein C.;

"mRNA sequences define an unusually restricted IgG response to 2-

"phenyloxazolone and its early diversification.";

Nature 304:320-324(1983).

-i- FUNCTION: Anti-2-phenyl oxazolone (FHOX) Antibody.
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Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
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Pred. No. 5.2e-33;
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13-AUG-1987 (Rel. 05, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
1g kappa chain V-VI region NQ5-61.1.2.
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                                                                                          (Rel. 05, Last sequence update) (Rel. 47, Last annotation update)
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                                               107 AA
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Interpro; IPR007110; Ig-like.
Interpro; IPR003596; Ig_V.
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Ig kappa chain V-VI region NQ6-8.3.1.
Mus musculus (Mouse).
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HSSP; P01679; 2FBJ.
                                               PRT;
                                                                               Created)
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1es 81, Conservative
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107
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PROSITE; PS50835; IG_L
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P04942;
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10-MAY-2005
                                                                               13-AUG-1987
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SEQUENCE
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Buropean Bioinformatics Institute. There are no restrictions on its as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                              23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR 82
                                                                                                                                                                                                                                                                                                                                           1 QILLIQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentía; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.; "Two murine natural polyreactive autoantibodies are encoded by
                                                                                                                                                                                                                                                                              Score 423; DB 1; Length 107;
Pred. No. 6.5e-33;
8; Mismatches 15; Indels
                                                                                                                                                               Complementarity-determining-1.
                                                                                                                                                                                      Complementarity-determining-2.
                                                                                                                                                                                                        Complementarity-determining-3. Framework-4.
                                                                                                                                      Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                            83 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKLE 126
                                                                                                                                                                                                                                                                                                                                                                                        61 FXGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGSGTKLE 104
                                                                                                                                                                                                                                                          11613 MW; A38290781F3C30D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
EMBL; AFS16285; AAM64203.1; -; Genomic_DNA.
PIR; PC4405; PC4405.
                                                                                                                                                                                                                                   By similarity.
                                                                           Ensembl; ENSMISSG0000062047; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insembl; ENSMUSG0000062047; Mus musculus
                                                                                                                                                                                                  Framework-3.
                                            EMBL; K00744; AAA38689.1; -; mRNA
HSSP; Q91W12; 1AY1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR00359; Ig-v.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                 64.5%;
                                                                                                                                                                                                                                                                                           77.98;
                                                                                                                             LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBK1F0 MOUSE PRELIMINARY;
Q8K1F0;
                                                                                                                                                                                                                                                                                           Best Local Similarity 77.9
Matches 81; Conservative
                                                                                                              SMART; SM00406; IGV; 1
PROSITE; PS50835; IG L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nonmutated germ-line
                                                                                                                                                                                                                                           107 1
107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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SMR; Q8K1F0; 3-112.
                                                                     SMR; P04944; 1-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10090;
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                                                          Q91W12;
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SEQUENCE
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25 VLSQSPAILFASPGETVTMTCRASSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTRFS 84
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                                                                                                                                                                                                                                    3 VI.TOSPAIMSASPGEKVIMICSASSSVSYMHWYQQKSGTSPKRWIYDTSKIASGVPARFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 VLSQSPAILPASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euronrognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "[Cloning and sequence analysis of the light chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
                                                                                                                        ö
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 immunoglobulin light chain variable region (Fragment).
                                                          Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
                                                                                                                     IndelB
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                                                                                                                                                                                                                                                                                                  GSGSGTSYSLTISRVEAEDAATYYCQOWSSNPFTFGSGTKLEI 127
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                                                                                                                                                                                                                                                                                                                                                          GSGSGNSYSLTISSTEGEDAATYYCQQWSSNPPTFGGGTKLEI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 GSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGSGTKLEI 127
112 AA; 11901 MW; F6644663201AA239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AA; 11478 MW; F20F544426BAE63E CRC64;
                                                       Query Match 64.3%; Score 422; DB 2; Best Local Similarity 80.6%; Pred. No. 8.5e-33; Matches 83; Conservative 3; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
64.2%; Score 421; DB 2,
Best Local Similarity 79.6%; Pred. No. 1e-32;
Matches 82; Conservative 8; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5, Last sequence update)
7, Last annotation update)
region NQ2-48.2.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF207620; AAF19434.1; -; Genomic_DNA.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; I-
PROSITE; PSS0835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9U410 MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-VI Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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10-MAY-2005 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12567627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huang H.L.,
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ID KV6G MOUSE
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                                                                                                                                         This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Clires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOI=10.1128/IAI.68.10.5803-5808.2000;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of
                                                               MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to
phenyloxazolone and its early diversification.";
Nature 304:320-324 [1983].
-i- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 420; DB 1; Length 107;
llarity 76.2%; Pred. No. 1.3e-32;
Conservative 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                          Framework-1.
Complementarity-determining-1.
Framework-2.
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                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-3.
Framework-4.
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                                                                                                                                                                                                                                                                                     PROSITE; PS50815; IG LIKE; 1.
Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                          11557 MW; 72488DA9EF354934 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 AA
                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
                                                                                                                                                                                                                             SMR; P04941; 1-103.
Ensembl; ENSMUSG0000062047; Mus musculus.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                       Framework-3.
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MEDLINE=20448942; PubMed=10992488;
                                                                                                                                                                                                          EMBL; K00737; AAA38682.1; -; mRNA.
HSSP; Q91W12; 1AY1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JL76 MOUSE PRELIMINARY;
Q9JL76;
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56
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97
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107
                                                        NUCLEOTIDE SEQUENCE
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nes 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                NCBI_TaxID=10090;
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SEQUENCE
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13-AUG-1987 (Rel. 05, Last sequence update)
10-MM-2005 (Rel. 07, Last annotation update)
10-MM-2005 (Rel. 07, Last annotation update)
11 Kappa chain V-V1 region NQ2-6.1.

Mus musculus (Mouse).

Rukaryota; Medazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Musinae; Mus.

NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LSASPGEKVTMTCRASSSVSYMFWYQQKPGSSPKPWIYATSNLASGVPARFSGSGSGTSY
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 LFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTRFSGSGSGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WUCLEOTIDE SEQUENCE.
MEDLINE=83271467; PubMed=6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRN sequences define an unusually restricted IgG response 'phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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                                                                                                                                                                                                                                                                                                                                                                               C9EE1FFE1F49DA1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 SLTISRVEAEDAATYYCQQWSSN-PFTFGSGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 419.5; DB : Pred. No. 1.3e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF206030; AAF6932808 (2000).
EMBL; AF206030; AAF69328.1; -; mRNA.
HSSP; P01679; 2F9J.
SMR; Q9176; 1-97J.
Ensembl; ENSWUSG0000057015; Mus musculus.
InterPro; IPR00710; IG-like.
InterPro; IPR003596; IG-V.
SMART; SM00406; IGV; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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SWR; P04945; 1-108.
Ensembl; ENSMUSG0000062686; Mus musculus.
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                               97 AA; 10542 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.5%;
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Matches 83; Conservative
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us-10-687-035-33.rup

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KV6B MOUSE
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P01675;
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NON TER
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                                                                                                   23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVLSQSPAILFASPGETVTMTCRASSSV--IYMCWNQQKPGSSPKPWIYGTSTLASGVPT
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paul
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                                                                                                                                             83 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNP--FTFGSGTKLEI 127
                                                                                                                                                          STRAIN=BALB/c; TISSUR=Hyperimmunized spleen;
Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y.,
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                               Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 408; DB 2; Length 114;
Pred. No. 1.9e-31;
6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8BD9833DBF3EEFD1 CRC64;
                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  Anti-VIPase light chain variable region (Fragment)
Mus musculus (Mouse).
                            Score 409; DB 1;
Pred. No. 1.5e-31;
                                                                                                                                                                                                                                               114 AA
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6; Mismatches
                                                        10; Mismatches
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PIR; A33933; A33933.
PIR; PH1058; PH1058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ensembl; ENSMUSG0000059896; Mus

    Exp. Med. 176:761-779(1992)

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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROSITE; PS50835; IG_LIKE; 1.
                             62.3%;
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l Similarity 78.3%;
83; Conservative
                                           Similarity 75.7
81; Conservative
                                                                                                                                                                                                                                             QBK1F1_MOUSE PRELIMINARY;
                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                    (TrEMBLrel.
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SWR; Q8K1F1; 2-114
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                            Query Match
Best Local 9
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This Swiss-Prot entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                   Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10 kappa chain V-VI region XRPC 24,
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                PROTEIN SEQUENCE.
MEDLINE=79082830; PubMed=103573;
Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
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107 AA
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; PO1679; 2FBJ.
SMR; PO1676; 1-107.
Ensembl; ENSMUSGO000062047; Mus musculus.
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                                                                                                                                                                                                              Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 17:5555-5559(1978)
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21-JUL-1986 (Rel. 01, Last seq
10-MAY-2005 (Rel. 47, Last ann
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nes 79; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=6776525;
Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
"Kappa Chain joining segments and structural diversity of antibody combining sites.";
Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
-I- MISCELLANBOUS: This chain was isolated from a myeloma protein that
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                            PROTEIN SEQUENCE.
MEDLINE-79082830; PubMed=103573;
Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.8%; Score 392; DB 1; Length 107; Best Local Similarity 74.3%; Pred. No. 6.3e-30; Matches 78; Conservative 8; Mismatches 19; Indels
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Complementarity-determining-3.
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PROSTTE; PS50835; IG LIKE; 1.
Inmunoglobulin V region. Framework-1.
REGION 24 33 Complementarity-detex REGION 34 48 Framework-2.
REGION 49 55 Complementarity-detex REGION 49 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
W -> I (in Ref. 2).
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HSSP; P01679; 2PBJ.
SMR; P01679; 1-107.
SMR; P01679; 1-107.
Interpro; IPR007110; Ig-like.
Interpro; IPR00359; Ig-v.
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                                                                                                                                     Biochemistry 17:5555-5559(1978)
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107 AA;
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REGION
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Search completed: March 20, 2006, 07:32:04 Job time : 25.7968 secs

8 B

Title: Perfect score:

Sequence:

protein

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Scoring table:

Searched:

Database

Result

Gaps

5

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A; Title: Immunoglobulin kappa light chain variable region gene complex organization and : A;Reference number: A94689; MUID:88331394; PMID:3138286
A,Accession: A32513
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-130 <KOF>
A,Cross-references: UNIPARC: UPI0000114D9C; GB:M20834; NID:g196943; PIDN:AAA38846.1; PID:; C;Superfeanily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;38-113/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m A;Reference number: 825057
A;Accession: 825058
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UP10000116096; EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology F;38-111/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDFQVQIPSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDPQVQIPSFLLISASVIMSRGQIVLTQSPAIMSASPGERVIMTCSASSSVSSSYLYWYQ
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C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 235;
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Pred. No. 1.4e-36;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                        Score 533; DB 2;
Pred. No. 6.7e-37;
                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%;
83.5%;
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.7%;
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain - mouse
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hes 106;
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                                                                                                                                              Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 3.Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: Ji.D679; A49044; B49044
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-real A;Reference number: JL0076; MUID:89096973; PMID:3211160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
432513

19 Ashapa chain precursor V region (MRL22) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Date: X: Strohal, R.; Balderas, R.S.; Johnson, M.B.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residue 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPARC;UPI000011E8E5; GB:S37664; NID:g250215; PIDN:AAB22332.1; PID: A;Experimental source: BALB/C germ-line A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit A;Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-25 AML5.
A;Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:9250214; PIDN:AAB22331.1; PID:
A;Note: gequence_extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JL0079
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: UNIPARC: UPI000017371F; GB:M27792; NID:g197159
A; Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A; Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A; Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 1
A; Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation R; Milstein, C; Even, J; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, B.
Bur J; Immunol. 22, 1627-1634, 1992
A; Title: Non-random features of the repertoire expressed by the members of one V kappa A; Reference number: A49044; MUID:92289826; PMID:1601044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 536; DB 1; Length 130;
Pred. No. 3.8e-37;
6; Mismatches 14; Indels
                       ALIGNMENTS
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84.1%;
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A; Introns: 17/1
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Best Local S:
Matches 106
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J. Biol. Chem. 264, 4513-4522, 1989
A;Title: Variable region primary structures of a high affinity anti-fluorescein immunogle A;Reference number: A32456; MUID:89174706; PMID:2494173
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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R;Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G.L.; Marken, J.S.; Aruffo,
J. Biol. Chem. 267, 15552-15558, 1992
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Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character
Reference number: A42848; MUID:92348410; PMID:1639794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 QKPGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDFLVQIFSFLLISASVAMSRGENVLTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSV--IYMCWNQ 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Mus musculus (house mouse)
Date: 27-Apr-1991 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                               989 #sequence_revision 26-Oct-1989 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss: Mus musculus (house mouse)
07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
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Pred. No. 9.5e-32;
5; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 501; DB 2;
Pred. No. 2.8e-34;
9; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;38-113/Domain: immunoglobulin homology <IMM>
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musculus (house mouse)
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Local Similarity 85.7%;
hes 90; Conservative
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Best Local Similarity 78.3%;
Matches 101; Conservative
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A; Residues: 1-130 < DOM>
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                 A; Residues: 1-130 cXOP.
A; Residues: 1-130 cXOP.
A; Residues: 1-130 cXOP.
A; Cross-references: UNIPARC:UPI0000115DFB; EMBL:X14620; NID:952031; PIDN:CAA32773.1; PID A; Cross-references: UNIPARC:UPI0000115DFB; EMBL:X14620; NID:952031; PIDN:CAA32773.1; PID C; Superfamily: immunoglobulin to codon AGC for residue 47 as Asn C; Superfamily: immunoglobulin immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
C; Keywords: heteroterramer; immunoglobulin predicted csIG>
F; 23-130/Product: Ig kappa chain V region (fragment) #status predicted cMAT>
F; 38-113/Domain: immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchd Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKPGSSPKPWIYGTSTLASGVPTRFSGSGSTSYSLTISRVEAEDAATYYCQQWSSNPFT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QRSGASPKLMIYGTSNLASGVPARFSGSGSGTSYSLTISSVBARDAATYYCQQYHSDPLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVBAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PDTSPKLMIYSTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPPTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDFQVQIFSFLLISASVIMTRGQIVLTQSPAIMSASPGEKVTWTCSASSSVSKYLNWYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDPQVQIFSPLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVI--YMCWNQ
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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;23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
;38-111/Domain: immunoglobulin homology <IMM>
;46-55/Region: complementarity-determining 1
;71-77/Region: complementarity-determining 2
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;130-140/Domain: constant region (fragment) #status predicted <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Cheng, H.L.; Sood, A.K.; Ward, R.B.; Kieber-Emmons, T.; Kohler, H.J. Immunol. 25, 33-40, 1988
Li Immunol. 25, 13-40, 1988
Title: Structural basis of stimulatory anti-idiotypic antibodies.
;Reference number: PLO011; MUID:88142863; PMID:3125424
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Pred. No. 2.1e-35;
6; Mismatches 16; Indel8
                                                                                                                                                                                                                                                                                                                                79.0%; Score 518; DB 2; Length 130;
80.6%; Pred. No. 1.1e-35;
ive 10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-140 «CHE>
Cross-references: UNIPARC:UPI00001767A6
Experimental source: cell line 4C11
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Best Local Similarity 82.7%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.6
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: PL0013
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                                                                                                                                                                                                                                                                                                                                   Query Match
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A; Accession: B30562
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R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
ArTitle: Structural characterization of antidiotypic antibodies; evidence that Ab2s are
A;Reference number: PLO080; MUID:89094248; PMID:2492056
A;Accession: PLO082
A;Accession: PLO082
A;Accession: 1-106 < MEES
A;Cross-references: UNIPARC;UPIO001767ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 1-132 <-LEV-
A,Residues: 1-132 <-LEV-
A,STRESIDUES: 1-132 <-LEV-
A,CTOGS-references: UNIPARC:UPI0000115DEC; EMBL:X14098; NID:g52562; PIDN:CAA32260.1; PID
R;Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
B. Exp. Med. 168, 1607-1620, 1988
A;Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explana
A,Reference number: JL0061; MUID:89035985; PMID:3141553
                                                                                                                                                                                                                                           A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclona (S.Superfamily: immunoglobulin V region; immunoglobulin homology (S.Superfamily: immunoglobulin immunoglobulin homology (F.Seywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FLLISVIVILINGEIFLTQSPAIIAASPGEKVTITCSASSSVSYMWYQQKFGSSPKIWI 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1g kappa chain precursor V-J region (18C13-V1) - mouse (fragment)
1g kappa chain precursor V-J region (18C13-V1) - mouse (fragment)
2;Species: Mus musculus (house mouse)
2;Species: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 21-Jan-2000
C;Accession: S05268; JL0062; S03846
R;Levy, S.
R;Levy, S.
A;Reference number: BMBL Data Library, February 1989
A;Reference number: S05267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIVLSQSPAILSASPGEKVTMTCRASSSVSYMNWYQQKPGSSPKPWESATSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.8%; Score 458; DB 2; Length 132; 76.3%; Pred. No. 9.2e-31; ive 10; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-120 <CAR>
A;Croses-references: UNIPARC:UPI0000176789; EMBL:X14098
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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F;109-132/Domain: J region (J-kappa-4) (fragment) <JRE>
                                                                                                                                                                                                                                                                                                                                                                            Score 462; DB 2;
Pred. No. 3.5e-31;
0; Mismatches 13;
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Ig kappa chain V region (27.10.2) – m
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                        A, Experimental source: strain BALB/c
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Best Local Similarity 87.6%;
Matches 92; Conservative
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Best Local Similarity 75...
Best Local 90; Conservative
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- mouse (fragment)

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C; Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C; Accession: B30562
R; Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L. J. Immunol. 142, 888-893, 1989
A; Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bir A; Reference number: A30562; MUID:89110066; PMID:2464031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-129 <KWA>
A;Cross-references: UNIPROT:P01680; UNIPARC:UPI000002A119; GB:V00780; NID:g51676; PIDN:C;
A;Note: the sequence was determined from the differentiated gene
C;Comment: This protein, in which there is a deletion of two amino acids at the V-J recon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 17/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into las
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKPGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEADDAATYYCQQWSSNPFT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor V region (S107B) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 QIVLSQSPAILFASPGETVIMICRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A01943
C;Accession: A01943
R;Kwan, S.P.; Max, B.E.; Seidman, J.G.; Leder, P.; Scharff, M.D.
R;Z, 57-66, 1981
A;Iitle: Two kappa immunoglobulin genes are expressed in the myeloma S107.
A;Reference number: A01943; MUID:82115300; PMID:6799208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Rosidues: 1-107 <SIK>
A;Cross-references: UNIPARC:UPI00001767BA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKLEI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
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Pred. No. 2.8e-30;
8; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 452; DB 2;
Pred. No. 2.3e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
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Best Local Similarity 74.4%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.98;
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Best Local Similarity 82.9°
Matches 87; Conservative
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Gaps

Length 104;

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A;Cross-references: UNIPARC:UP10000115F57; EMBL:X59094; NID:g5227; PIDN:CAA41820.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-88/Domain: immunoglobulin homology <IMM>
. Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antige ance number: A49049; MUID:93049629; PMID:1425914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: PC4405
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
R;Denges Biochem. J. 12, 448-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire A;Reference number: PC4405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QIVLTQSPAIMSASPGEKVIMTCSASSSVSYMHWYQQXSGTSPKRWIYDTSKLTSGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
Accession: S29591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR
                                                                                                                                                                                                                          A;Note: Bequence extracted from NCBI backbone (NCBIN:118298, NC C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin homology c;Keywords: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 FSGSGSGTSYSLTISRVEAEDAATYYCOOWSSNPFTFGSGTKLE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSGSGSTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 104
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                                                                                                                                                                                                                                                                                                                                                                       Score 438; DB 2;
Pred, No. 3.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 437; DB 2;
Pred. No. 3.8e-29;
5; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, April 1991
A,Reference number: S26459
A,Accession: S29591
                                                                                                                                            A;Residues: 1-104 <ARM>
A;Cross-references: UNIPARC:UP100001767AD
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C:Superfamily: immunoglobulin V re
                                                                                                                                                                                                                                                                                                                                                                             66.8%;
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ilarity 82.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        81.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 81.73
Matches 85; Conservative
                                                                                                                                                                                                     A; Experimental source: BALB/c
                                                                                                                 A; Molecule type: nucleic acid
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-103 < KAV>
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A; Residues: 1-107 <DEN>
                                                                                      A;Status: preliminary
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19 kappa chain V region (35.8.2H) - mouse (fragment)

C;Species: Mar-1989 #aquence_revision 23-Mar-1989 #text_change 21-Jan-2000

C;Accession: G30560

R;Matsuda, T.; Kabat, E.A.

J. Immunol. 142, 863-870, 1989

A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclo
                                                                                                                                                                                               J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A;Reference number: A30562; MUID:89110066; PMID:2464031
                                                                                                        C;Date: 23.Mar-1989 #sequence_revision 23.Mar-1989 #text_change 21-Jan-2000
C;Accession: A30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I
J. Immunol. 142, 888-893, 1989
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C;Species: Mus musculus (house mouse)
C;Decies: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49049
C;Accession: B4049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Bur. J. Immunol. 22, 2893-2899, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 448; DB 2; Length 107;
Pred. No. 4.9e-30;
5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: G30560
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
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                                                        Ig kappa chain V regions (27.7.2 and 27.4b.2)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPARC: UP100001767B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 68.3%;
1 Similarity 82.9%;
87; Conservative
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Best Local Similarity 83.0%;
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
                                                                                                                                                                                                                                                                                      A; Accession: A30562
A; Status: preliminary
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Best Local S
Matches 87
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Length 103;

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Ristark, S.B.; Caton, A.J.
L. Exp. Mad. 114, 613-624 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein el
A;Reference number: S26309; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: FT0406
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded anti-DNA autoantibodi A;Reference number: PT0376; MUID:91147903; PMID:1900082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI0000115F82; EMBL:X59197; NID:g52328; PIDN:CAA41907.1; PID C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-89/Domain: immunoglobulin homology <IMM>
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C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                                 Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QIVLTQSPAIMSASPGEKVTISCSASSSVSYMYWYQQKPGSSPKPWIYRTSNLASGVPAR
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A;Cross-references: UNIPARC:UPI00001767E8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Koywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
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                          PSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPVTFGAPTKLEL 105
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Pred. No. 9.8e-29;
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ilarity 81.0%;
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Matches 85; Conserv
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A;Residues: 1-105 <STA>
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submitted to the EMBL Data Library, November 1993
A;Reference number: $38713
A;Reference number: $38713
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-108 <CIM>
A;Cross-references: UNIPARC:UPI0000117544; EMBL:X76023; NID:9416104; PIDN:CAA53610.1; PI
C;Superfemily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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PS0071
Ig kappa chain V region (38C13.V8) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: PS0071
R;Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A;Title: Punctional immunoglobulin light chain genes are replaced by ongoing rea A;Artile: Punctional immunoglobulin light chain genes are replaced by ongoing rea A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Accession: PS0071
A;Acatus: translation not shown
A;Molecule type: DNA
A;Residues: 1-106 <LEV>
A;Cross-references: UNIPARC:UPI00001767C9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
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                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                 Ig light chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38720
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Pred. No. 5.7e-29;
6; Mismatches 14; Indels
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Pred. No. 3.9e-29;
4; Mismatches 15;
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Pred. No. 5.2e-29;
8; Mismatches 12.
  F;16-89/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 81.0%;
Matches 85; Conservative
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1 MDFQVQIPSFLLISASVIMS......YCQQWSSNPFTFGSGTKLEI 127
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2: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
      GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 100 summaries
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Sequence 135, App
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APPLICANT: Neges Technologies, Inc.
APPLICANT: Degrees, Shawn
APPLICANT: Degrees, Shawn
APPLICANT: Degrees, Shawn
APPLICANT: David
APPLICANT: Bayer: Robert
APPLICANT: Bayer: Robert
APPLICANT: Bowe, Caryn
APPLICANT: Hakes, David
APPLICANT: Gove, Caryn
APPLICANT: Hakes, David
APPLICANT: Hakes, David
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APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANTON NUMBER: US/11/183,205
CURRENT APPLICATION NUMBER: US 60/334,233
PRIOR FILING DATE: 2005-07-15
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2002-07-15
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-06-16
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89.8%; Pred. No. 6.6e-38;
iive 2; Mismatches 11; Indels
US-11-102-621-135
US-11-174-186-7
                                                                                                                                    ALIGNMENTS
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                                                                                                                                                                                                                                                                                         Sequence 60, Application US/11183205; Publication No. US20060030521A1; GENERAL INFORMATION:
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ORGANISM: Mus musculus
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US-11-250-411-87
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APPLICANT: HANGARAR, Vinay
APPLICANT: HANGARAR, Vinay
APPLICANT: HO, Sun
APPLICANT: HO, Sun
APPLICANT: HO, Sun
APPLICANT: HO, Sun
APPLICANT: LAW, Debbie
TITLE OF INVENTION: USE OF ANTI ALPHASBETA1 ANTIBODIES TO INHIBIT CANCER CELL
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: PROLIFERATION
TITLE OF INVENTION: DAGE: 2056,03.34
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/556,422
PRIOR APPLICATION NUMBER: 60/556,422
PRIOR APPLICATION NUMBER: 60/655,049
PRIOR APPLICATION NUMBER: 60/651,098
PRIOR PILING DATE: 2004-01-03
PRIOR APPLICATION NUMBER: 60/651,514
PRIOR PRILING DATE: 2005-02-07
PRIOR PRILING DATE: 2005-02-07
PRIOR PRILING DATE: 2005-02-07
PRIOR PRILING DATE: 2005-02-08
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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APPLICANT: RAMADA, YOKO
APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: NAKAWURA, KAZUYASU
APPLICANT: SHEWYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/19/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR PLING DATE: 1999-05-20
PRIOR PLING DATE: 1999-05-20
PRIOR PLING DATE: 1999-05-20
PRIOR PLING DATE: 1999-11-21
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1997-11-21
SOFTWARE: PALENTIN NUMBER: PCT/JP97/04259
PRIOR PLING DATE: 1997-11-21
SOFTWARE: PALENTIN VOICE: 2.1
SOFTWARE: PALENTIN VOICE: 2.1
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Publication No. US20050260210A1
GENERAL INFORMATION:
APPLICANT: PROTEIN DESIGN LABS, INC.
APPLICANT: RAMAKRISHNAN, Vanitha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
HANAI, NOBUO
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121 AGTKLEL 127
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121 FGGGTKLEI 129
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APPLICANT: RAMAKRISHNAN, Vanitha
APPLICANT: RAMAKRISHNAN, Vanitha
APPLICANT: BHASKAR, Vinay
APPLICANT: HASKAR, Vinay
APPLICANT: HO, Sun
APPLICANT: LAW, Debbie
APPLICANT: LAW, Debbie
ITILE OF INVENTION: USE OF ANTI ALPHASBETA1 ANTIBODIES TO INHIBIT CANCER CELL
ITILE OF INVENTION: PROLIFERATION
ITILE OF INVENTION: PROLIFERATION
ITILE OF INVENTION WUMBER: US/11/090,331
CURRENT FILING DATE: 2005-03-24
RRIOR APPLICATION NUMBER: 60/556,421
RRIOR FILING DATE: 2004-03-24
PRIOR PILING DATE: 2004-03-24
PRIOR PLILING DATE: 2004-11-03
PRIOR PLILING DATE: 2004-11-03
PRIOR PLILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: 60/651,098
PRIOR PLILING DATE: 2005-02-07
PRIOR PLILING DATE: 2005-02-07
PRIOR PLILING DATE: 2005-02-28
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                                                                                                                                                 75.3%; Score 494; DB 7; Length 130; 79.1%; Pred. No. 6.9e-32;
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Pred. No. 7.3e-32;
7; Mismatches 18;
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US-11-090-331-8
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Publication No. US20050260210A1
GENERAL INFORMATION:
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Best Local Similarity 79.1%;
Matches 102; Conservative .
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SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 138
                                                                                                                                               Query Match
Best Local Similarity 79.13
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FGGTKLEI 129
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                                                ; TYPE: PRT
; ORGANISM: mus muscalus
US-11-090-331-4
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SEQ ID NO 4
LENGTH: 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SGTSPKLLIYRTSNLASGVPFRFSGSGSGTFYSLTISSVEAEDAADYYCHQWSM--YTFG 118
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                                                                                                                                                                                                                                                                            1 MDFQVQIFSFLLISASVIMSRGQIVLTQSPAIMSASLGEBITLTCSASSSVSYMHWYQQK 60
                                                                                                                                                                                                                                          1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein US-11-250-411-89
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                                                                                                Query Match 72.9%; Score 478; DB 7; Length 126; Best Local Similarity 78.7%; Pred. No. 1.2e-30; Matches 100; Conservative 6; Mismatches 19; Indels
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TITLE OF INVENTION: OPTIMIZED FC VARIANTS
FILE REFERENCE: A-71366-9
CURRENT PELING DATE: 2005-05-05
CURRENT PILING DATE: 2005-05-05
PRIOR PELING DATE: 2004-07-15
PRIOR FLING DATE: 2004-07-15
PRIOR FLING DATE: 2004-07-20
PRIOR FLING DATE: 2004-07-20
PRIOR PLING DATE: 2004-01-09
PRIOR PLING DATE: 2004-11-09
PRIOR PLING DATE: 2004-11-09
PRIOR PLING DATE: 2004-11-10
PRIOR PLING DATE: 2004-11-10
PRIOR PLING DATE: 2004-11-10
PRIOR PLING DATE: 2004-01-13
PRIOR PLING DATE: 2004-01-14
PRIOR PLING DATE: 2004-01-15
PRIOR PLING DATE: 2004-01-16
PRIOR PLING DATE: 2004-03-66
PRIOR PLING DATE: 2004-03-66
PRIOR PLING DATE: 2004-03-66
PRIOR PLING DATE: 2004-03-66
PRIOR PLING DATE: 2003-03
PRIOR PLING DATE: 2003-09-26
PRIOR PLING DATE: 2003-09-36
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APPLICANT: Lazar, Gregory Alan APPLICANT: Dang, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Desjarlais, John R. APPLICANT: Karki, Sher Bahadur APPLICANT: Vafa, Omid APPLICANT: Hayes, Robert
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SGTKLEI 127
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Matches 93; Conserva
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US-11-124-620-6
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RESULT 8

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65 PKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTK 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 SFLLISASVIM----SRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSS
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GENERAL INFORMATION:
FUDILICATION NO. US20060024300A1
GENERAL INFORMATION:
APPLICATION OF US20060024300A1
FILE REPERENCE: P1990R3C1P1
CURRENT ADPLICATION NUMBER: US/11/190,364
CURRENT APPLICATION NUMBER: US/11/190,364
CURRENT APPLICATION NUMBER: US 60/434,115
FRIOR PILING DATE: 2002-07-26
FRIOR PILING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-01
FRIOR PLING DATE: 2003-12-01
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR PLING DATE: 2003-12-16
FRIOR APPLICATION NUMBER: US 11/147,780
FRIOR PLING DATE: 2003-05-06-07
FRIOR PLING DATE: 2005-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.4%; Score 475; DB 7; Length 236; 78.9%; Pred. No. 3.3e-30; ive 4; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.4%; Score 475; DB 7; Length 236; Best Local Similarity 78.9%; Pred. No. 3.3e-30; Matches 97; Conservative 4; Mismatches 18; Indels
Sequence 19, Application US/11106820
Publication No. US2006002930a1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G
APPLICANT: SEMELL, KATHRYN L.
ITTLE OF INVENTION: Treatment of Disorders
FILE REPRENCE: P2102R1
CURRENT APPLICATION NUMBER: US/11/106,820
CURRENT FILING DATE: 2005-04-15
PRIOR PPLICATION NUMBER: US 60/563,227
PRIOR PPLICATION NUMBER: US 60/565,098
PRIOR APPLICATION NUMBER: US 60/565,098
PRIOR APPLICATION NUMBER: US 60/565,098
PRIOR PILING DATE: 2004-04-16
PRIOR PILING DATE: 2004-04-16
PRIOR SEQ ID NOS: 45
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: sequence is synthesized
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.99
Matches 97; Conservative
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Length 106;

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                                                                 66 PKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVBABDAATYYCOOWSFNPPTFGAGTK 125
6 AFLLASMFVFSIATNAYAQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AFLLASMFVFSIATNAYAQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSS
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                                                                                                                                                                                                                                                                      Sequence 17, Application US/11147780

Publication No. US20060034835A1

GENERAL INFORMATION:

APPLICANT: Adams ET AL.

TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof

FILE REPRENCE: P1990R3C1

CURRENT APPLICATION NUMBER: US/11/147,780

CURRENT FILING DATE: 2005-06-07

PRIOR APPLICATION NUMBER: US 60/434,115

PRIOR APPLICATION NUMBER: US 60/526,163

PRIOR PILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-12-01

PRIOR FILING DATE: 2003-12-16

PRIOR FILING DATE: 2003-12-16

NUMBER OF SEQ ID NOS: 38

SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 236;
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APPLICANT: GONG, QIAN
APPLICANT: GONG, QIAN
APPLICANT: MAKTIN, FLAVIUS
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT PILING DATE: 2005-04-15
PRIOR APPLICANION NUMBER: US 60/563,263
PRIOR PILING DATE: 2004-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , DB 7;
3.3e-30;
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Pred. No. 3
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US-11-147-780-17
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Publication No. US20050276803A1
GENERAL INFORMATION:
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78.9%;
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.9
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 52
SEQ ID NO 28
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US-11-107-028-28
                                                                                                                             125 LBI 127
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1 QIVLSQSPAILSASPGEKVTWTCRASSSVSYMHWYQQKPGSSPKPWIYAPSNLASGVPAR 60
                                                                                                                            1 QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYAPSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKPWIYGTSTLASGVPTR 82
                                              O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                               83 PSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKLEI 127
                                                                                                                                                                                                                                        FSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFGAGTKLEL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFGSGTKLEI 127
, DB 7;
4.2e-30;
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Pred. No. 4.2e-30;
2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BRUNETTA, PAUL G
APPLICANT: SEWELL, KATHRYN L.
TITLE OF INVENTION: Treatment of Disorders
TITLE OF INVENTION: Treatment of Disorders
CURRENT APPLICATION NUMBER: US/11/106,820
CURRENT FILING DATE: 2005-04-15
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 45
LENGTH: 107
Score 470; DE
Pred. No. 4.2e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GRENAL, IQBAL S.
APPLICANT: WALICKE, PATRICIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DIS
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR PILING DATE: 2004-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/11106820 Publication No. US20060002930A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/11120338
Publication No. US20050271658A1
                                                                                             23 QIVLSQSPAILFASPGETVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.6%;
Matches 92; Conservative
Query Match 71.6%;
Best Local Similarity 87.6%;
Matches 92; Conservative
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1 Similarity 87.6%;
92; Conservative
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SEQ ID NO 1
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mus musculus US-11-120-338-1
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Best Local Similarity
Matches 92; Conserv
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1 QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYAPSNLASGVPAR 60
1 QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYAPSNLASGVPAR 60
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                                                                                                                                                                                                                                    Sequence 1. Application US/11147780
; bublication No. US2066034835A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; PILE REFERENCE: P1990R3C1
; CURRENT FILING DATE: 2005-06-07
; PRIOR FILING DATE: 2005-06-07
; PRIOR FILING DATE: 2002-12-16
; PRIOR PLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 2003-12-01
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 1
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Pred. No. 4.2e-30;
2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
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                                                                                                       PSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFGAGTKLEL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 FSGSGSGTSYSLTISRVEAEDAATYYCQOWSSNPFTFGSGTKLEI 127
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Publication No. US20060051345A1
GENERAL INFORMATION:
APPLICANT: FROHMA, PAUL A.
TITLE OF INVENTION: METHOD FOR TREATING MULTIPLE SCLEROSIS
FILE REPRENCE: P2134R1
CURRENT APPLICATION NUMBER: US/11/143,386
CURRENT FILING DATE: 2005-06-02
PRIOR FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 25
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Pred. No. 4.2e-30;
2; Mismatches 11;
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71.6%;
Best Local Similarity 87.6%;
Matches 92; Conservative 7
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ilarity 87.6%;
Conservative
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CRCANISM: Mus musculus
US-11-143-386-1
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US-11-147-780-1
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Best Local Similarity
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LENGTH: 107
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Matches
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                                  1 QIVLSQSPAILSASPGEKVTWTCRASSSVSYMHWYQQKPGSSPKPWIYAPSNLASGVPAR 60
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| Publication No. US20060024300A1
| GENERAL INPORMATION:
| APPLICANT: Adams ET AL.
| TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
| FILE REPERENCE: P1990R3CLP1
| CURRENT FILING DATE: 2005-07-26
| PRIOR PPPLICATION NUMBER: US/11/190,364
| CURRENT FILING DATE: 2002-12-16
| PRIOR FILING DATE: 2002-12-16
| PRIOR PPLICATION NUMBER: US 60/526,163
| PRIOR PPLICATION NUMBER: US 60/526,163
| PRIOR PPLICATION NUMBER: US 11/197,780
| PRIOR FILING DATE: 2003-12-16
| PRIOR FILING DATE: 2003-12-16
| PRIOR FILING DATE: 2003-12-16
| PRIOR FILING DATE: 2003-12-16
| PRIOR FILING DATE: 2003-12-16
| PRIOR FILING DATE: 2003-13-16
| PRIOR FILING DATE: 2003-13-16
| PRIOR FILING DATE: 2003-06-07
| NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 71.6%; Score 470; DB 7; Length 107; 1 Similarity 87.6%; Pred. No. 4.2e-30; 92; Conservative 2; Mismatches 11; Indels
                                                                                                                                    61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFGAGTKLEL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFGAGTKLEL 105
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                                                                                                                                                                                                                                                                         Sequence 1, Application US/11143077
Publication No. US20060024295A1
GENERAL INCRMATION:
TITLE OF INVENTION: WETHOD FOR TREATING LUPUS
FILE REFERENCE: P2133R1
CURRENT APPLICATION NUMBER: US/11/143,077
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US 60/577,235
PRIOR APPLICATION NUMBER: US 60/577,235
PRIOR PILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/617,997
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
Matches 92; Conserv
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TYPE: PRT
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61 PGKAPKLLIYDTSKLPSGVPSRPSGSGSGTDFTLTISSLQPEDFATYYCQQMSSNPPTFG 120
                APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-HUMAN VEGF RECEPTOR FLT-1 MONDER: 249-107
CURRENT PAPLICATION NUMBER: US/09/453,718
PRIOR PPLICATION NUMBER: US/09/453,718
PRIOR PELING DATE: 1999-12-03
PRIOR PPLICATION NUMBER: 09/119,014
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR PPLING DATE: 1999-05-20
PRIOR PELING DATE: 1999-11-21
NUMBER OF SEQ ID NOS: 111
SEQ ID NO 92
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDFQVQIPSFLLISASVIISRGDIQMTQSPSSLSASVGDRVTITCSASSSVSYMHWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein US-11-250-411-92
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; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: GONG, QIAN
; APPLICANT: GONG, QIAN
; TILLE REPERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT PILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 128;
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Best Local Similarity 72.4%; Pred. No. 2e-29;
Matches 92; Conservative 13; Mismatches 22; Indele
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SEQ ID NOS: 52
IENGTH: 106
TYPE: PRT
PREATURE: PRT
PREATURE: Artificial sequence
PRATURE: ORGANISM: Sequence is synthesized
US-11-107-028-34
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity
Matches 90; Conserva
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                                                                                                                              23 QIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQKPGSSPKFWIYGTSTLASGVPJ
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/11/193,440

FILING DATE: 01-Aug-2005
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGBNT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
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Pred. No. 7.1e-30;
0; Mismatches 12
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ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-11-193-440-89
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STREET: 1300 I Street, NW
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Publication No. US20060034838A1
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SEQUENCE CHARACTERISTICS
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Best Local Similarity 88.6'
Matches 93; Conservative
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Search completed: March 20, 2006, 07:32:42 Job time : 3.37968 secs

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                                                                                                                                            US-11-089-367-11

US-11-089-367-11

US-10-627-556-214

US-10-627-556-244

US-10-207-655-154

US-10-053-530-34

US-11-089-190-34

US-11-089-510-34

US-11-089-570-34

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- 2006 Biocceleration Ltd.
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US-11-089-511-11
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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(c) 1993
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Maximum DB seq length: 200000000
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                                                                              Copyright
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Match
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Database

Result No.

Title: Perfect

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| APPLICANT: MA, JING
| APPLICANT: MA, JING
| APPLICANT: GUO, Yajun
| TITLE OF INVENTION: PREPARATION AND APPLICATION OF
| TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
| FILE REFERENCE: 549062000200
| CURRENT APPLICATION NUMBER: US/10/723,003
| CURRENT FILING DATE: 2003-11-26
| PRIOR PILING DATE: 2003-11-25
| PRIOR PILING DATE: 2003-11-25
| PRIOR FILING DATE: 2003-6-13
| NUMBER OF SEQ ID NOS: 68
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 129
| WANDER OF SEQ ID NOS: 68
| LENGTH: 129
                                                                                                        Sequence 33, Application US/10687035
| Sequence 33, Application US/10687035
| Publication No. US20050064518A1
| GENERAL INPORMATION:
| APPLICANT: Albone, Earl F. |
| APPLICANT: Soltis, Daniel A. |
| TITLE OF INVENTION: ANTHRODIES THAT BIND CELL-ASSOCIATED |
| TITLE OF INVENTION: ANTHRODIES THAT BIND CELL-ASSOCIATED |
| TITLE OF INVENTION: ANTHRODIES THAT BIND CELL-ASSOCIATED |
| TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF |
| FILE REFERENCE: 6750-214-999 |
| CURRENT FILING DATE: 2003-10-15 |
| PRIOR FILING DATE: 2003-07-10 |
| PRIOR FILING DATE: 2003-07-10 |
| PRIOR FILING DATE: 2003-10-15 |
| NUMBER OF SEQ ID NOS: 71 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 33 |
| LENGTH: 127
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100.0%; Pred. No. 5.9e-49;
tive 0; Mismatches 0;
ALIGNMENTS
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. Sequence 38 Application US/10723003
. Publication No. US20040254108A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 127; Conservative
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Length 129;

88.1%; Score 578; DB 5;

US-10-723-003-38

Query Match

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Sublication No. US20050232931A1

GENERAL INFORMATION:

APPLICANT: M. M. Jing

APPLICANT: GUO, Yajun

TITLE OF INVENTION: PREPARATION AND APPLICATION OF

TITLE OF INVENTION: ANIT-TUMOR BIFUNCTIONAL FUSION PROTEINS

FILE REFERENCE: 549052002000

CURRENT PILING DATE: 2004-12-02

PRIOR APPLICATION NUMBER: US/11/04,639

CURRENT PILING DATE: 2003-11-26

PRIOR PILING DATE: 2003-11-26

PRIOR PILING DATE: 2003-11-25

PRIOR FILING DATE: 2003-11-25

PRIOR PRILING DATE: 2003-11-25

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PRIOR PILING DATE: 2003-11-25

PRIOR PRILING ING DATE: 2003-11-25

PRIOR PRING PRING DATE: 2003-11-25

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Pred. No. 3.2e-42;
2; Mismatches 10; Indels
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Publication No. US20040254108A1
GENERAL INFORMATION:
APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
APPLICANT: GUO, Yajun
APPLICANT: GUO, Yajun
APPLICANT: GUO, Yajun
APPLICANT: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REPRENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT PELICATION NUMBER: CM 2003-11-26
PRIOR PILING DATE: 2003-11-25
Best Local Similarity 90.6%; Pred. No. 3.2e-42;
Matches 115; Conservative 2; Mismatches 10; Indels
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Best Local Similarity 90.6%;
Matches 115; Conservative
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US-11-004-639-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SGTKLEI 127
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDPQVQIFSFLLISASVIMSRGQIVLSQSPAILSASPGEKVTWTCRASSSVSYIHWPQOK 60
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Sequence 42, Application US/11004639
Rublication No. US20050232931A1
SEQUENCE INFORMATION:
APPLICANT: WA, JING
ITIER OF INVENTION: PREPARATION AND APPLICATION OF
ITIER OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION FROTEINS
FILE REFERENCE: 54906200020
CURRENT APPLICATION NUMBER: US/11/004,639
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US/10/723,003
PRIOR PILING DATE: 2003-11-25
PRIOR PELING DATE: 2003-11-25
PRIOR PLILING DATE: 2003-11-25
PRIOR PILING DATE: 2003-11-25
PRIOR PILING DATE: 2003-16-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 235
TYPE: PRI
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                       Query Match 88.1%; Score 578; DB 5; Length 235; Best Local Similarity 90.6%; Pred. No. 5.9e-42; Matches 115; Conservative 2; Mismatches 10; Indels
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PRIOR APPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 42
LENGTH: 235
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                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic Construct US-10-723-003-42
                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SGTKLEI 127
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APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John B.
APPLICANT: Leonard, John B.
APPLICANT: Reff, Mitchell B.
APPLICANT: Reff, Mitchell B.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricte
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lym
VUMBER OF SEQUENCES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DAIR:
PLICATION WHERE: US/09/905,928 FILING DAIR: 17-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 572; DB 3
Pred. No. 1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/475,813
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/149,099
PILING DATE: 03-NOV-1993
PRICH APPLICATION NUMBER: US 08/149,099
PILING DATE: 03-NOV-1993
PRICH APPLICATION NUMBER: US 07/978,891
PILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: TESKIN, RODIN I.
REGISTRATION NUMBER: 35,030
REFREENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAK: 703-836-2001
. Anderson, Darrell R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.2%;
89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.2
Best Local Similarity 89.8
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-905-928-4
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22314
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SGTKLEI 127
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Sequence 60, Application US/10411037

Sequence 60, Application US/10411037

Sequence 60, Application US/20040043446A1

GENERAL INFORMATION:

APPLICANT: Neces Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Robert

APPLICANT: Bayer, Shawn

APPLICANT: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

TITLE OF INVENTION: GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA

TITLE OF TILNG DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07

PRIOR FILING DATE: 2002-06-07
                                                                                             APPLICANT: ANDRESON, DAKKELL R.
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: BENNARD, JOÉN E.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: REFF, MITCHELLE
TITLE OF INVENTION: THERAPETTIC APPLICATION OF CHIMERIC AND RADIOLABELED
TITLE OF INVENTION: THERAPETTIC APPLICATION OF CHIMERIC AND RADIOLABELED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION UNMER: US/10/238,681
CURRENT PILING DATE: 1995-08-29
PRIOR FILING DATE: 1995-08-29
PRIOR FILING DATE: 1995-11-03
PRIOR APPLICATION NUMBER: 08/149,099
PRIOR FILING DATE: 1992-11-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
INNERT PATENTION OF CELL
SEQ ID NO 7
INNERT PATENTION OF CELL
TITLE OF INVENTION NUMBER: 07/978,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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87.2%; Score 572; DB 4; Length 128;
Best Local Similarity 89.8%; Pred. No. 1e-41;
Matches 114; Conservative 2; Mismatches 11; Indels
Sequence 7, Application US/10238681 Publication No. US20030147885A1 GENERAL INFORMATION:
                                                                                 APPLICANT: ANDERSON, DARRELL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGTKLEI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Murine sp. US-10-238-681-7
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                                                                                                                                                                                                   Leonard, John B.
Newman, Roland A.
Reff, Mitchell B.
Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
Radiolabeled Antibodies to Human B Lymphocyte Restricted
Differentiation Antigen for the Treatment of B-Cell Lymphom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/096,964
FILING DATE: 14-Mar-2002
CLASSIFICATION: 4Unknown>
PRIOR APPLICATION: 4Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/475,813
FILING DATE: 07-JUN-1993
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN D.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                            Sequence 4, Application US/10096964
Publication No. US20030082172A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 703-836-6620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
                                                                                                                                                                                    Hanna, Nabil
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Best Local Similarity 89.8
Matches 114; Conservative
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      RESULT 7
US-10-096-964-4
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61 PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
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                                                                                                                      61 PGSSPKPWIYGTSTLASGVPTRFSGSGSTSYSLTISRVBAEDAATYYCQQWSSNPFTFG 120
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           1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60
                                                            1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTWTCRASSSVSYIHWFQQK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chen, Xi
PEDLICANT: Bowe, Caryn
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 572; DB 4
Pred. No. 1e-41;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-20
PRIOR FILING DATE: 2002-06-15
PRIOR FILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
SROFWARE: PATENTING DATE: 2002-08-18
SUFFWARE: PATENTING DATE: 2002-08-18
SUFFWARE: PATENTING DATE: 2002-08-18
SUFFWARE: PATENTING DATE: 2002-08-18
SUFFWARE: PATENTING DATE: 2002-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 040853-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
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PRIOR FILING DATE: 2001-10-10
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Publication No. US20040082026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.8%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus musculus
US-10-410-962-60
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US-10-411-049-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS
FILE REPRESENCE: 040853-01-5058
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGSSPKPMIYATSNIASGVPVRPSGSGSGTSYSLTISRVEAEDAATYYCQOWTSNPPTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDFQVQIPSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
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2; Mismatches 11; Indels
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PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-007-17
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
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89.8%; Pred. No. 1
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PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR PILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
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No. US20040063911A1
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
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Best Local Similarity 89.8
Matches 114; Conservative
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Best Local Similarity 89.8
Matches 114; Conservative
                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-411-037-60
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; ORGANISM: Mus musculus
US-10-411-026-60
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LENGTH: 126
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APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA
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Pred. No. 1e-41;
2; Mismatches 11; Indels
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Pred. No. 1e-41;
2; Mismatches 11; Indels
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CURRENT APPLICATION NUMBER: US/10/410,930
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SEQ ID NOS: 75
SEQ ID NOS: 75
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Gene, Caryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60, Application US/10410930 Publication No. US20040115168A1 GENERAL INFORMATION:
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89.8%;
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Best Local Similarity 89.8%;
Matches 114; Conservative
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Best Local Similarity 89.8<sup>†</sup>
Matches 114; Conservative
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 128
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; ORGANISM: Mus musculus
US-10-410-930-60
                                                                                                                                TYPE: PRT
CRGANISM: Mus musculus
US-10-327-663-12
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121 GGTKLEI 127
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APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERPERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
FILE REPERBNCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR PELING DATE: 2001-10-10
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-66-07
PRIOR PELING DATE: 2002-66-07
PRIOR PELING DATE: 2002-66-07
PRIOR PELING DATE: 2002-66-16
PRIOR APPLICATION NUMBER: US 60/301,777
PRIOR PELING DATE: 2002-66-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PELING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PELING DATE: 2002-08-16
PRIOR PELING DATE: 2002-08-16
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APPLICANT: Kenya SHUTARA
APPLICANT: Kenya SHUTARA
APPLICANT: Kenya UGHIDA
APPLICANT: Kenya UGHIDA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Toyohide SHINKAWA
APPLICANT: Mitsuo SATOH
APPLICANT: Ryosuke NAKANO
TITLE OF INVENTION: ANTIBODY COMPOSITION WHICH SPECIFICALLY BINDS TO CD20
FILE REFERENCE: 249-289
CURRENT APPLICATION NUMBER: US/10/327,663
CURRENT APPLICATION NUMBER: UP 2001-392753
FRIOR APPLICATION NUMBER: JP 2001-392753
FRIOR APPLICATION NUMBER: JP 2002-106948
FRIOR PILING DATE: 2002-04-09
FRIOR FILING DATE: 2002-04-09
FRIOR FILING DATE: 2001-11-01
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                                APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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Matches 114; Conservative
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US-10-411-049-60
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   GENERAL INFORMATION:
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APPLICANT: Chen, X1
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: GIYCOPECYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: GIYCOPECYLATION METHODS
FILE REPERENCE: 040653-01-5051
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PLING DATE: 2001-10-10
PRIOR PLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/347,592
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PLING DATE: 2002-06-07
PRIOR PLING DATE: 2002-06-25
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-06-16
PRIOR PLING DATE: 2002-07-17
PRIOR PLING DATE: 2002-07-17
PRIOR PLING DATE: 2002-07-17
PRIOR PLING DATE: 2002-08-16
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TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REPERENCE: 04083-01-5052-00
CURRENT APPLICATION NUMBER: US/10/287,994
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/324,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-0-10
PRIOR FILING DATE: US 60/387,292
PRIOR FILING DATE: US 60/391,777
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Pred. No. 1e-41;
2; Mismatches
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FILING DATE: 2002-06-25
APPLICATION NUMBER: US 60/396,594
FILING DATE: 2002-07-17
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o. US20040137557A1
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Best Local Similarity 89.8%;
Matches 114; Conservative
      Hakes, David
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US-10-411-012-60
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APPLICANT: Bowe, Caryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: FSH
FILE REFERENCE: 040853-01-5059
FURRENT APPLICATION NUMBER: US/10/410,997
CURRENT APPLICATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
61 PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYVCQQWTSNPPTFG 120
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PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR PILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-10-19

PRIOR PILING DATE: 2002-06-07

PRIOR PILING DATE: 2002-06-07

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PRIOR PILING DATE: 2002-08-16

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SEQ ID NOS: 75

SEQ ID NO 60

LENGTH: 128
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Publication No. US20040132640A1
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Neose Technologies,
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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US-10-410-997-60
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121 GGTKLEI 127
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GABREAL INCOMMATION:
APPLICANT: Nocae Technologies, Inc.
APPLICANT: DeFrees, Shawn
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APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
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APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Said
APPLICANT: Bayer, Solarid
APPLICANTON: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
FILE REFRERENCE: 04063-01-506
CURRENT FILING DATE: 2003-04-09
PRIOR FILING DATE: 2001-10-10
PRIOR PLILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-25
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PRIOR PLING DATE: 2002-08-38
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PRIOR PLING 
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1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK
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GENERAL INFORMATION: APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60, Application US/10410980 Publication No. US20050031584A1 GENERAL INFORMATION:
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Best Local Similarity 89.84
Matches 114; Conservative
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US-10-410-980-60
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US-10-410-897-60
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APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
FILE OF INVENTION: METHODS
FILE OF INVENTION: METHODS
FILE OF INVENTION: MOMBER: US 6/328,523
FRIOR APPLICATION NUMBER: US 6/328,523
FRIOR FILING DATE: 2001-10-10
FRIOR PRILING DATE: 2001-10-19
FRIOR FILING DATE: 2002-06-05
FRIOR APPLICATION NUMBER: US 60/387,292
FRIOR PRILING DATE: 2002-06-25
FRIOR PRILING DATE: 2002-06-25
FRIOR PLILING DATE: 2002-07-17
FRIOR FILING DATE: 2002-07-17
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Pred. No. 1e-41;
2; Mismatches 11; Indels
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89.8%; Pred. No. 1e-41;
tive 2; Mismatches 11; Indels
   PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR PILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOPTWARE: Petentin version 3.1
SEQ ID NO 60
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Publication No. US20040142856A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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89.8%;
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APPLICANT: SOPE, David
APPLICANT: Haker, Robert
APPLICANT: Haker, David
APPLICANT: Chen, Xi
TITI:P
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Best Local Similarity 89.83
Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
US-10-287-994-60
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ORGANISM: Mus musculus
US-10-410-913-60
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Best Local Similarity
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1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60

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APPLICANT: ZOPÉ, DATA

APPLICANT: BANET, ROBERT

APPLICANT: BANET, ROBERT

APPLICANT: BOWE, CALTA

APPLICANT: BOWE, CALTA

APPLICANT: BOWE, CALTA

FILE REPERRICE: 040833-01-5058

CURRENT PPLIAN NUMBER: US 60/328,523

PRIOR PELICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR PLIANG DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR PLIANG DATE: 2002-08-28

PRIOR PLIANG DATE: 2002-08-28

PRIOR PLIANG DATE: 2002-08-28

PRIOR PLIANG DATE: 2002-08-28

NUMBER OF SEQ ID NOG: 75

SOFTWARE: PRIOR PLIANG DATE: 2002-08-28

NUMBER OF SEQ ID NOG: 75

SEQ ID NO 60

LENGTH: 128

TYPE: PRI

COMMANDER: PRIOR PRIOR NUMBER: US 60/407,527

PRIOR PLIANG DATE: 2002-08-28

NUMBER OF SEQ ID NOG: 75

SEQ ID NO 60

LENGTH: 128

TYPE: PRI

COMMANDER: PRIOR PRIOR NUMBER: US 60/407,527

PRIOR PLIANG DATE: 2002-08-28

NUMBER OF SEQ ID NOG: 75

SEQ ID NO 60

LENGTH: 128

TYPE: PRI

COMMANDER: PRIOR PRIOR NUMBER: US 60/407,527

PRIOR PLIANG DATE: 2002-08-28

NUMBER OF SEQ ID NOG: 75

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 Db
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US-08-438-528-2
US-08-438-528-3
US-08-43-278-31
US-08-477-728-31
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Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

APPLICANT: Anderson, Darrell R.

APPLICANT: Anderson, John E.

APPLICANT: Reff, Mitchell E.

APPLICANT: Reff, Mitchell E.

APPLICANT: Rastetter, William H.

TITLE OF INVENTION: Therapeutic Application of Chimeric and

TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell

TITLE OF INVENTION: Lymphoma

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ANTHER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
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COMPUTER: THE PC Compatible
SOCTHARE: BEACHLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-040-1995
CLASSIFICATION NUMBER: US/08/476,275
FILING DATE: 07-040-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 012712-155
TELECOMMUNICATION NUMBER: 012712-155
TELECOMMUNICATION NUMBER: 012712-155
TELECOMMUNICATION NUMBER: 012712-155
TELEFRAX: 703-836-6620
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ALIGNMENTS
                                                                                                      Sequence 4, Application US/08476275
Patent No. 5776456
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 89.8
Matches 114; Conservative
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Alexandria
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                                                                                                                                              APPLICANT: ANDERSON, DARRELL R.
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
APPLICANT: HANNAD, JOHN E.
APPLICANT: NEWMAN, TOLAND B.
APPLICANT: REFF, MITCHELL B.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: PREAPENTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: LYMPHOMA
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: PILLSBURY WINTHROP
STREET: 1100 New YORK Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
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89.8%; Pred. No. 3.2e-50;
tive 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 03-NOV-1993
PRIOR APPLICATION NUMBER: 08 07/978,891
PRILING DATE: 13-NOV-1992
ATTORNEY, AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 235.22-0157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 860 ID NO: 7:
SEQUENCE CHRACATERISTICS:
Sequence 7, Application US/08475815B Patent No. 6399061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New York Avenue, CITY: Washington STATE: DC COUNTRY: USA ZIP: 20005 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING SYSTEM: PC-DOS/MS-DC OPERATING
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Best Local Similarity 89.8'
Matches 114; Conservative
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to Human B Cell Surface Anti-

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Ledbetter, Jeffrey
ENTION: Chimeric Antibody with Specificity
CE: PPL-001CN2
                                             APLICANI: LeadesCree, Jenieriey
TILLE REFERENCE: PPL-001CN2
CURRENT APPLICATION NUMBER: US/09/724,138
CURRENT APPLICATION NUMBER: US/09/724,138
CURRENT APPLICATION NUMBER: US/09/724,138
PRIOR PILING DATE: 2000-08-01
PRIOR FILING DATE: 1998-02-12
PRIOR PILING DATE: 1998-06-06
PRIOR PILING DATE: 1998-06-06
PRIOR PILING DATE: 1998-06-06
PRIOR PILING DATE: 1998-06-06
PRIOR PILING DATE: 1998-06-06
PRIOR PILING DATE: 1988-06-13
PRIOR PILING DATE: 1988-05-13
PRIOR PILING DATE: 1988-05-13
PRIOR PILING DATE: 1988-05-13
PRIOR PILING DATE: 1988-05-13
PRIOR PILING DATE: 1986-05-13
PRIOR PILING DATE: 1986-05-13
PRIOR PILING DATE: 1986-10-07
NUMBER OF SEQ ID NOS: 50
SOUTWARE: Patentin version 3.0
SEG ID NO 46
LEMOTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SGTKLEI 127
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121 AGTKLEL 127
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                                                   APPLICANT: Anderson, Darrell R.
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell B.
APPLICANT: Rafetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,813
FILING DATE: 07-000-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-000-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-000-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPRENCY NUMBER: 35,030
REPRENCY NUMBER: 35,030
REPRENCY NUMBER: 35,030
REPRENCY NUMBER: 35,030
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REPRENCY NUMBER: 35,030
REPRENCY NUMBER: 35,030
RELECTION NUMBER: 35,030
RELECTION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22314
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-724-138-46
; Sequence 46, Application US/09724138
; Patent No. 6652852
; GENERAL INFORMATION:
Sequence 4, Application US/08475813
Patent No. 6682734
GENERAL INFORMATION:
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amino acid
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ADDRESSEE: BURNS, DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-475-813-4
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APPLICANT: Robinson, Randy
APPLICANT: Liu, Alvin
APPLICANT: Ledbetter. Jeffrey
TITLE OF INVENTION: Chimeric Antibody with Specificity to Human B Cell Surface Antic
FILE REFERENCE: PPL-001CN
                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVRAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PGSSPKPWIYAPSNLASGVPARPSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFG 120
                                                                                                                                                                                                                                                                                                           1 MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTWTCRASSSVSYMFWYQQK 60
                                                                                                                                                                                                                                                                 1 MDFQVQIPSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                    Length 128;
                                                                                                             Query Match

86.3%; Score 566; DB 2;
Best Local Similarity 88.2%; Pred. No. 1.3e-49;
Matches 112; Conservative 4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APLICANI: LEGGRECUES, JELLIEY
FILE REFERENCE: Chimeric Antibody with
FILE REFERENCE: PPL-001CN
CURRENT APPLICATION WUMBER: US/09/630,198
CURRENT TILNG DATE: 2000-08-01
PRIOR PILING DATE: 1998-02-12
PRIOR FILING DATE: 1998-06-06
PRIOR FILING DATE: 1998-06-06
PRIOR FILING DATE: 1991-03-05
PRIOR FILING DATE: 1991-03-05
PRIOR FILING DATE: 1991-03-05
PRIOR FILING DATE: 1991-03-05
PRIOR FILING DATE: 1991-03-05
PRIOR FILING DATE: 1988-05-13
PRIOR FILING DATE: 1986-05-13
PRIOR FILING DATE: 1986-05-03
PRIOR FILING DATE: 1986-01-08
PRIOR FILING DATE: 1986-01-08
PRIOR FILING DATE: 1986-01-08
PRIOR FILING DATE: 1986-10-08
PRIOR FILING DATE: 1986-10-08
PRIOR FILING DATE: 1986-10-08
PRIOR FILING DATE: 1986-10-08
PRIOR FILING DATE: 1986-10-08
PRIOR FILING DATE: 1986-10-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-09-630-198-46
Sequence 46, Application US/09630198
Patent No. 6893625
GENERAL INFORMATION:
; ORGANISM: Mus musculus
US-09-724-138-46
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121 SGTKLEI 127
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   linear
TOPOLOGY:
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                                                                                                                                                                                                    Length 128;
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Sequence 2, Application US/08449287

Sequence 2, Application US/08449287

Sequence 2, Application US/08449287

Sequence 2, Application US/08449287

Sequence 2, Application US/08449287

APPLICANT: ADAIR, John Robert

APPLICANT: BODMER, Mark William

APPLICANT: BODMER, Mark William

APPLICANT: OWENS, Raymond John

TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and

TITLE OF INVENTION: Their Production

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: IBM PC compatible

COMFUTER: IBM PC compatible

CONFUME: PatentIn Release #1.0, Version #1.25

SOFFWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

APPLICATION UNMBER: 08/154,389
                                                                                                                                                                                        Score 566; DB 2;
Pred. No. 1.3e-49;
4; Mismatches 11;
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BETNHARD DATA:
NAME: SAXE, BETNHARD OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF ST
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
                                                                                                                                                                                                86.3%;
88.2%;
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(202) 672-5399
                                                                                                                                                                                                Query Match
Best Local Similarity 88.2
Matches 112; Conservative
       ; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-630-198-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTKLEI 127
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                                                                                                                                                                                                                                                        61 PGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFG 120
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                                                                                                                                              1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK
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                                                         Length 129;
                                                                                                      14; Indels
                                                           Score 559; DB 1;
Pred. No. 6.6e-49;
1; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
FILING DATE: 09-No. 6339070-1999
FILING DATE: 05-MAY-1998
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pillsbury Winthrop, L
STREET: 1100 New York Ave., N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
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Patent No. 6339070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 235 amino acids TYPE: amino acid
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                                                           Query Match 85.2%;
Best Local Similarity 88.2%;
Matches 112; Conservative
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Best Local Similarity 88.24
Matches 112; Conservative
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MOLECULE TYPE: protein US-08-449-287-2
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61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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APPLICANT: HANNA, NABIL
APPLICANT: HARINARNI, KANDASAMY
APPLICANT: HARINARNI, KANDASAMY
APPLICANT: HOYNH, TRI B.
TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
FILE REFERENCE: 2352.0584
CURRENT APPLICATION NUMBER: US/09/238,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVT
                                                                      ADDRESSEE: Pillsbury Madison & Sutro, LLP
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Pred. No. 1.4e-48;
1; Mismatches 14
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIPTCATION **CURRENTS**
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SECTION OC: 23:
                                                                                                              CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
                                                                                            STREET: 1100 New York Ave., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-011-769A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09238741
Patent No. 6897044
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.2
Matches 112; Conservative
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SEQ ID NO 2
LENGTH: 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: MS WORD
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                 APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.I
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
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                                                                                                                                                                   Application US/09423439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 235 amino acids
TYPE: amino acid
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MARSHAM, Peter R.
DOWELL, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
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DAVIES,
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121 SGTKLEI 127
                                          121 GGTKLEI 127
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61 PGSSPKPWIYGTSTLASGVPTRFSGSGGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 548; DB 4; Length 128;
Pred. No. 8.4e-48;
6; Mismatches 12; Indels
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/259,963
FILING DATE: 14-UNNE-94
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REJESTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9507302 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPAtible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 85.8°
Matches 109; Conservative
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                                                                                                                                                    SGTKLEI 127
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US-07-946-421-26
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                                                                                                                                                                                                                                     1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQK 60
                                                                                                                                                                                              1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2. Application US/08619491

Patent No. 6210670

GENERAL INFORMATION:

PAPPLICANT: BEST9, Ellen L.

TITLE OF INVENTION: Specific for E-Selectin and P-Selectin

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTY: 10.5A
                                                                                                                                                      ö
                        ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: "Dimeric" Anti-CD20 Light Chain (Version 1)
US-09-238-741-2
                                                                                                             Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 128;
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                                                                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patent BM PC compatible
CORRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,491
FILING DATE: 26-MAR-1996
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/07302
FILING DATE: 107-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,963
FILING DATE: 14-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.5%; Score 548; DB 2;
85.8%; Pred. No. 8.4e-48;
tive 6; Mismatches 12;
                                                                                                        85.1%; Score 558; DB 2;
88.2%; Pred. No. 1.7e-48;
tive 2; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 011823-005810US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Storella, John R. REGISTRATION NUMBER: 32,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
                                                                                                           Query Match
Best Local Similarity 88.2
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.8
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-08-619-491-2
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1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60

Gaps

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61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVBAEDAATYYCQQWSSNPFTFG 120
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                  3: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Woodcock Masburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Ploor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 543; DB 1; Length 235;
Pred. No. 5.7e-47;
5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,569B
FILING DATE: OT-SEP-1994
CLASSIFICATION:
ATTONENY/AGBRT INFORMATION:
NAME: TTUJI110, DOTEON Yako
REGISTRATION NUMBER: 35,719
REFRENCE/DOCKET NUMBER: 35,719
REFRENCE/DOCKET NUMBER: 35,719
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE (TARACTERISTICS:
LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08116247
Patent No. 5929212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.0%;
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Best Local Similarity 85.0
Matches 108; Conservative
                                                             CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDPQVQIPSFLLISASVILSRGQIVLTQSPAIMSASPGEKVTMTCSASSSVTYMYWYQQK 60
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                                      GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Kettleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                E: Millen, White, Zelano & Branigan, P.C. 2200 Clarendon Boulevard, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised Antibodies
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Patent No. 5852205
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: BRIAGE, John S.
TITLE OP INVENTION: Humanised Antib
NUMBER OF SEQUENCES: 31
Sequence 26, Application US/07946421
                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: U.S.A.
21F: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 128 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-303-569B-5
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Query Match
Best Local Similarity 85.0%;
Matches 108; Conservative
                                                  235 amino acids
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SEQ ID NO 5
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-795-515-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 SGTKLEI 127
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                                                                         amino acid
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ORGANISM: Mouse
US-09-348-224-5
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                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDFQVQIFSFLLISASVIISRGQIVLTQSPAIMSASPGEKVTWTCSASSSVSYMWYQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09795515
Sequence 5. Application US/09795515
Settent No. 6632927
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.8%; Score 543; DB 1; Length 235; Best Local Similarity 85.0%; Pred. No. 5.7e-47; Matches 108; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAC COMPATIBLE
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 35,719
TELECOMMUNICATION INFORMATION:
TELECHONE: (215) 568-3439
                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PTLING DATE: 10-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: 19,386
TELEFOMMUNICATION INFORMATION:
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3100
TELEFAX: (215) 568-3101
TELEFAX: (215) 568-3101
TELEFAX: (215) 568-3101
TELEFAX: (215) 568-3101
TELEFAX: (215) 568-3101
TELEFAX: (215) 568-3101
TELEFAX: (215) 368-3101
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TELEFAX: (215) 368-3101
TELEFAX: (215) 368-3101
TELEFAX: (215) 368-3101
                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-116-247-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One Libert;
CITY: Philadelphia
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61 PGSSPKPWIYGTSTLASGVPTRPSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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                                                                                                                                   1 MDFQVQIFSFLLISASVIISRGQIVLTQSPAIMSASPGEKVTMTCSASSSVSYMNWYQQK 60
                                                                                                        1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                        Gaps
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Pred. No. 5.7e-47;
5; Mismatches 14; Indels
Query Match
82.8%; Score 543; DB 2; Length 235;
Best Local Similarity 85.0%; Pred. No. 5.7e-47;
Matches 108; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09348224

Sequence 5, Application US/09348224

Sequence 10. 6750325

GENERAL INFORMATION:

APPLICANT: Joining Kay

APPLICANT: Adair, John Robert

APPLICANT: Athwal, Diljeet Singh

TITLE OF INVENTION UNUBER: US/09/348,224

CURRENT FALLION NUMBER: US/09/348,224

CURRENT FILING DATE: 1999-07-06

EARLIER APPLICATION NUMBER: 08/116,247

EARLIER APPLICATION NUMBER: 09/116,247

EARLIER APPLICATION NUMBER: 09/743,377

EARLIER APPLICATION NUMBER: 07/743,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
US-08-116-778E-2
; Sequence 2, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUXASU
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61 PGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRWEAEDAATYYCQQRSSYPYTFG 120
61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVRAEDAATYYCQQWSSNPPTFG 120
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WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
CONSENSUS
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OD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
OD: CONSENSUS
/product= "HYPERVARIABLE REGION 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR PATELOATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REFERENCE/POCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF STOLEMATICS:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
TENERAL 129 amino acids
                                                                                                                                                                                                                                                                                                                               APPLICANT: NARAWURA, KAZUYASU
APPLICANT: NARAWURA, KAZUYASU
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : NIXON & VANDERHYB P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                 Sequence 2, Application US/08438562
Patent No. 5874255
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NAME/KEY: domain
LOCATION: 24..33
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IDENTIFICATION METHOD: V
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                                                                                                121 SGTKLBI 127
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STATE: VIRGINIA
COUNTRY: U.S.A.
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WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
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WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
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LOCATION: 24..33
LDENTIFICATION METHOD: BY SIMILARITY
LDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ES
LDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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LOCATION: 49..55
LDENTIPICATION METHOD: BY SIMILARITY
LDENTIPICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTIMENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
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LOCATION: 88..96
LDENTIFICATION METHOD: BY SIMILARITY
LDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTIMENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
                                                                                                                                                                                                                                                                 STATE: VINGINAL
COMPUTRY: U.S.A.
ZIP: 22201-4714

COMPUTRY: U.S.A.
COMPUTRR READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTRI: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION DATA: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
RECISTRATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
TELEPAX: (703) 816-4100
TELEPAX: 129 amino acids
'PWCTH: 129 amino acids
                                                                  APPLICANT: KUMNA, YOSHIHISA
PEDLICANT: HASGEAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESSES: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                           SHITARA, KENYA
HANAI, NOBUO
KUWANA, YOSHIHISA
    KOIKE, MASAMICHI
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TYPE: amino acid
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LOCATION: -22...1
IDENTIFICATION METHOD: B
IDENTIFICATION METHOD: I
IDENTIFICATION METHOD: (
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Best Local Similarity 84.3
Matches 107; Conservative
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MOLECULE TYPE: protein
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Search completed: March 20, 2006, 07:31:34 Job time: 7.76331 secs
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                                                                         NAME/KEY: domain

LOCATION: 88..96

IDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED

IDENTIFICATION METHOD: CONSENSUS

OTHER PROPERATION: /product= "HYDERVARIABLE REGION 3"

US-08-438-562-2
                                                                                                                                                                                                                                                                     81.1%; Score 532; DB 1; Length 129; 84.3%; Pred. No. 3.5e-46; tive 6; Mismatches 14; Indels
IDENTIFICATION METHOD: CONSENSUS OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 07-JUN 95 CLASSIFICATION: 536 CLASSIFICATION: TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFAX: (703)816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MANAGONA MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: KUWANA, WAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
CORRESPONDENCES: 103
CORRESPONDENCE ADDRESS: 103
CORRESPONDENCE ADDRESS: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
US-08-483-528B-92
i Sequence 92, Application US/08483528B
i Sequence 92, Application US/08483528B
i Setent No. 5939532
i GENERAL INFORMATION:
i APPLICANT: NAKAWURA, KAZUYASU
i APPLICANT: SHIYRA, KENYA
APPLICANT: SHIYRA, KENYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703)816-4100
INFORMATION FOR SEQ 1D NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
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LOCATION: -22...1
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
FEATURE:
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Best Local Similarity 84.3
Matches 107; Conservative
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MOLECULE TYPE: protein
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61 PGSSPKPWIYGTSTLASGVPTRF8GSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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LOCATION: 49..55
LDENTIFICATION METHOD: BY SIMILARITY
LDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
LDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: domain

LOCATION: 88.-296

LIDENTIFICATION METHOD: BY SIMILARITY

IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED

IDENTIFICATION METHOD: CONSENSUS

CHER INFORMATION: /product= "HYPERVARIABLE REGION 3"

US-08-483-528B-92
                                            BY SIMILARITY WITH KNOWN SEQUENCE OR TO AN ESTABLISHED CONSENSUS
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84.3%; Pred. No. 3.5e-46;
tive 6; Mismatches 14; Indels
                     LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESIDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
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Best Local Similarity 84.3*
Matches 107; Conservative
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GenCore version 5.1.7
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March 20, 2006, 07:28:19 ; Search time 45.9655 Seconds
 (without alignments)
1213.978 Million cell updates/sec Run on:

US-10-687-035-33 656 1 MDPQVQIPSFLLISASVIMS......YCQQWSSNPPTFGSGTKLEI 127 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2443163 Total number of hits satisfying chosen parameters: 2443163 seqs, 439378781 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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1: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
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7: geneseqp2003s:\*
8: geneseqp2003bs:\*
9: geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Ad894334	ADD82234 Ady21925 Ady70628 Aap94781 Aaw10243 Aaw10589
SUMMARIES	ADS94334 AAR15323 AAR33127 ADV92494 ADV99557 ADV99561 ADV99657 ADV99661 AAR55214 ABR55872 AAR55872 AAR55872 ADC6268 ADE8686 ADE8686 ADR9730 ADV7408 ADV759908 ADV759908 ADV559908 AAC59908 AAC59908 AAC59908	ABB82834 ADY21925 AAP70628 AAP94781 AAW10243
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\$ Query Match Length	0.00 0.00	86.3 86.3 86.3 86.3 86.3
Score	6 5 5 6 5 6 5 6 5 6 5 6 5 6 5 6 6 6 6 6	566 566 566 566 566
Result No.	10646668886618846618	20 21 23 23 24 24

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The present invention describes an isolated antibody, or an antigen-
binding antibody fragment (1), that preferentially binds cell-associated
CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also
cascribed: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
a monoclonal antibody that competes with binding of (II); (3) a hybridoma
CC amposited in (II); (4) an isolated nucleic acid molecule (III)
comprising a nucleotide sequence that encodes a variable chain region of
C(1); (5) a pharmaceutical composition comprising an antibody or an
antigen-binding antibody fragment that preferentially binds cell-
associated CA 125/0772P polypeptide relative to shed CA 125/0772P
C(1); (5) a pharmaceutical composition comprising a
monoclonal antibody or an antigen-binding monoclonal antibody fragment
CC that preferentially binds cell-associated CA 125/0772P polypeptide, and a carrier; (7) an article
CM manufacture (IV) comprising packaging material and a composition
CC of manufacture (IV) comprising packaging material and a composition
CC comprising an antibody, or an antigen-binding antibody fragment that
CC comprising an antigen-binding antibody fragment that
CC composition in a form suitable for administration to a subject; (8) a
C125/0772P relative to shed CA 125/0772P pelative to shed CA
CC composition in a form suitable for administration to a subject; (8) a
C125/0772P relative to shed CA 125/0772P operably linked to a heterologous
CC composition in a form suitable for administration to a subject; (8) a
C125/0772P relative to shed CA 125/0772P operably linked to a heterologous
CC 2125/0772P relative to shed CA 125/0772P relative to shed CA
CC 125/0772P relative to shed CA 125/0772P operably linked to a heterologous
CC 3125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P relative to shed CA 125/0772P 
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                                                                                                                                                                                                                                                                                                                                                                                                     antibody; antigen-binding antibody fragment; cell-associated CA 125/0772P; monoclonal antibody; cytostatic; immunostimulant; mediator of lysis; tumour; cell proliferative disorder; cancer; cervical cancer; uterine cancer; breast cancer; lung cancer; ovarian cancer.
Ady21789 Antibody
Ady21653 Antibody
Ady21933 Antibody
                                                                                                                                                                                                                                                                                                                                                         Antibody 776.1 light chain variable region (776.1L) SEQ ID NO:33
                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 32; SEQ ID NO 33; 153pp; English.
  ADY21789
ADY21653
ADY21933
                                                                                                                                                                                                                            ADS94334 standard; protein; 127 AA
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    200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-357171/33.
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    86.3
86.3
86.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
    566
566
566
                                                                                                                                                                                                                                                                        ADS94334;
                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                         ADS94334
    98
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antibody fragment; (11) an antibody or antigen binding antibody fragment; that competes with (11), and (12) a pharmaceutical composition comprising (VI) and a carrier. (1) has cytostatic activity, and can be used as an immunostimulant and a mediator of lysis of positive tumour cell. (1) is useful for ameliorating a symptom of a CA 125/O7P-related disorder which is a cell proliferative disorder such as cancer, cervical or uterine cancer, breast or lung cancer or ovarian cancer. (V) is useful diagnostically for monitoring the development or progression of cancer or tumour as part of clinical testing procedure. The present sequence represents an antibody light chain variable region amino acid sequence which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK
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100.0%; Score 656; DB 8;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 127; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. .22
'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL-2 chimeric antibody light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR15323 standard; protein; 145 AA.
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/note= "C-region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-2; immunosuppressant.
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(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                          Sequence 127 AA;
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25-MAR-2003
16-MAR-1992
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AAR15323
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WPI; 1991-363168/50

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61 PGSSPKFWIQATSNIAFGVPSRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                         This sequence is from the light chain variable region of an anti-IL2R alpha monoclonal antibody. The antibody is only weakly inhibitory on its own. When anti-IL2R alpha antibodies which are strongly inhibitory on their own are used with anti-CD4 antibodies which are also strongly inhibitory, their immunosuppressive properties are improved; they synergistically inhibit T-helper cell proliferation to effectively inhibit transplant rejection at low doses without significantly reducing the general immune response. No such synergistic effect is observed with the weakly inhibitory MAD M-215. See AAQ36607-Q36616. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointestinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                   se as immunosuppressant - comprises .. monoclonal anti-IL2R alpha- or anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Mature 2B8 light chain variable region protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDFQVQIFSFLLISASVIMSRGKIVLSQSPAILSASPGEKVTMTCRASSSISYMHWYQQK
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

88.3%; Score 579; DB 2;
Best Local Similarity 89.8%; Pred. No. 6.2e-35;
Matches 114; Conservative 4; Mismatches 9.
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/label= Signal peptide
                                   Synergistic antibody compsn. for use monoclonal anti-CD4 antibodies and mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                             Sxample 1; Page 15; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADV92494 standard; protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2003; 2003CN-00129290.
25-NOV-2003; 2003CN-01119930.
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/note= "L
23. .129
                                                                         IL2R beta antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SGTKLEM 127
N-PSDB; AAQ36613.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 145 AA;
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
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                                                                                                                           The sequence is that of the interleukin-2 (IL-2) chimeric antibody light chain, coded by clone 215. Antibodies against IL-2 receptors are useful as immunosuppressants, and are much less immunosuppressants are useful antibodies. See also ARMIS321-RIS326. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                   New recombinant DNA encoding chimeric antibody - with human constant and non-human variable regions, esp. directed against interleukin 2 receptor
                                                                                                                                                                                                                                                                                                                                                                                    1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                Score 579; DB 2; Length 145;
Pred. No. 6.2e-35;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-IL2R-alpha antibody M-215 light chain variable region
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/label= J4-region
129. .145
/label= start_of_Constant_region
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/label= Variable-region
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                                                                                         Disclosure; Page 12; 24pp; German
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/label= signal
                                                                                                                                                                                                                                                                                  88.3%;
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(first entry)
                                                                                                                                                                                                                                                                                                                      Matches 114; Conservative
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
N-PSDB; AAQ15115
                                                                                                                                                                                                                                            Sequence 145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1991;
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10-MAR-2003
02-JUN-1993
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RESULT 3 AAR32127

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Gaps

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N-PSDB; ADV98556
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(GUOY/) GUO Y.
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                                                                                                                     The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the 2B8 light chain variable region
                                                                                                                                                                                                                                                                                                       PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                   New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
                                                                                                                                                                                                                                                        MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein engineering, pharmaceutical, cytostatic, vaccine, cancer, neoplasm, melanoma, breast tumor, hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel chimeric protein-related 2B8 light chain protein SeqID38
                                                                                                                                                                                                                 Score 578; DB 9; Length 129;
Pred. No. 6.5e-35;
2; Mismatches 10; Indels
                                                                                                     Claim 23; SEQ ID NO 38; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYMB-) SYMBIGENE ACQUISITION CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                  ADV98557 standard; protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-2003; 2003CN-00129290.
25-NOV-2003; 2003CN-01119930.
26-NOV-2003; 2003US-00723003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-2003; 2003CN-01119930.
26-NOV-2003; 2003US-00723003.
28-NOV-2003; 2003TW-00133577.
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                                                                                                                                                                                                                     88.18;
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                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.6
Matches 115; Conservative
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                                     2005-030218/03.
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                                              N-PSDB; ADV92493
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(GUOY/) GUO Y.
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                  Guo Y;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody engineering; chimeric antibody; cytostatic; gene therapy; vaccine; gastrointeetinal disease; immune response; melanoma; malignancy; breast cancer; hepatocellular carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PGSSPKPWIYATSNIASGVPVRF8GSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEABDAATYYCQQWSSNPFTFG 120
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New chimeric protein for preventing or treating neoplastic conditions, e.g. melanoma, breast cancer or hepatocellular carcinoma, comprises an Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
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130. .235
/note= "Human kappa chain constant cDNA (CL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.1%; Score 578; DB 9;
90.6%; Pred. No. 6.5e-35;
iive 2; Mismatches 10
                                                                                                                                                                    Example 5; SEQ ID NO 38; 147pp; English.
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/label= Signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADV92498 standard; protein; 235 AA.
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25-NOV-2003; 2003CN-01119930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-2003; 2003US-00723003
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Matches 115; Conserv
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Flt3 ligand or its fragment, and a proteinuous or peptidyl tumoricidal
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                                                                                                                                                                                                                                                                                                                  121 SGTKLEI 127
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N-PSDB; AAQ65630.
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Best Local Similarity
                                                                                                                                   of the invention
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                                                                                                                                                         Sequence 235 AA;
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01-FEB-1995
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                                                                                                                    The present invention relates to a chimeric protein having a Flt3 ligand (FL) or its biologically active fragment and a proteinuous or peptidyl tumoricidal agent. The invention is useful for treating malignancy, neoplasm e.g. melanoma, breast cancer, hepatocellular carcinoma and as a vaccine for eliciting an immune response. The invention is also useful in gene therapy. The present sequence is the anti-CD20 chimeric antibody
                                                                                                                                                                                                                                                                                                                                         PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
                                                                                                                                                                                                                                                                                                                            PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                      9
                                                    New chimeric protein comprises an Flt3 ligand and a proteinuous or peptidyl tumoricidal agent, useful for treating malignancy or neoplasm, e.g. melanoma, breast cancer, or hepatocellular carcinoma.
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                                                                                                                                                                                                                                                                                               MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQK
                                                                                                                                                                                                                                                                                 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel chimeric protein-related anti-CD20 light chain protein SeqID42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein engineering; pharmaceutical; cytostatic; vaccine; cancer; neoplasm; melanoma; breast tumor; hepatocellular carcinoma.
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                                                                                                                                                                                                                                   88.1%; Score 578; DB 9; Length 235; 90.6%; Pred. No. 1.2e-34; ive 2; Mismatches 10; Indels
                                                                                                  Claim 23; SEQ ID NO 42; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYMB-) SYMBIGENE ACQUISITION CO INC.
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; 2003CN-01119930.
; 2003US-00723003.
; 2003TW-00133577.
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                      2005-030218/03
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                                                                                                                                                                                        chain protein
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Matches 115; Conserv
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                                                                                                                                                                                                               Sequence 235 AA;
                                N-PSDB; ADV92497
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 Guo Y:
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28-NOV-2003;
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This invention relates to a novel chimeric protein comprising an Flt3 ligand, or its biological fragment, and a proteinuous or peptidyl tumoricidal agent. The invention may be useful for the production of compounds with a cytostatic activity or a vaccine. The composition and methods are useful for preventing or treating neoplastic conditions, such as melanoma, breast cancer or hepatocellular carcinoma. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PGSSPKPWIYATSNIASGVPVRFSGSGSGTSYSLTISRVEAEDATYYCQQWTSNPPTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 578; DB 9;
Pred. No. 1.2e-34;
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ID NO 42; 147pp; English
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93US-00149099
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90.6%;
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WPI; 2003-352746/33
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                                                                                                                                              PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                 9
murine anti-CD20 monoclonal antibody 2BS. See also AAQ65629-35. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                               remodeling; glycoconjugation; glycosyltransferase; glycan; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a cell-free, in vitro method of remodeling a peptide. The method involves removing a saccharyl subunit from the peptide, thus forming a truncated glycan, and contacting the truncated glycan with at least one glycosyltransferase and at least one glycosyl anor under conditions suitable to transfer at least one glycosyl donor
                                                                                                            1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                              Gaps
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                                                            Length 128;
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                                                                            11; Indels
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                                                          Score 572; DB 2;
Pred. No. 1.8e-34;
2; Mismatches 11;
                                                                                                                                                                                                                                                                                            Anti-CD20 antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Накев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowe C,
                                                                                                                                                                                                                                       ABR55872 standard; protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 82B; 900pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bayer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0344692P.
2001US-0334233P.
2001US-0334301P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2002; 2002US-0387292P.
25-JUN-2002; 2002US-0391777P.
17-JUL-2002; 2002US-0396594P.
16-AUG-2002; 2002US-0404249P.
                                                          87.2%;
89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-0407527P
                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2002; 2002WO-US032263
                                                                                                                                                                                                                                                                           (first entry)
                                                                      Best Local Similarity 89.8
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zopf D,
                                                                                                                                                                                          127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-449162/42.
N-PSDB; ACC78894.
                                                                                                                                                                         SGTKLEI 127
                                                                                                                                                                                         GGTKLEI
                                           Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                       antibody; mouse.
                                                                                                                                                                                                                                                                                                                                                            402003031464-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-2001;
28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2002;
                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2001;
                                                                                                                                                                                                                                                                           02-SEP-2003
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                                                                                                                                     61
                                                                                                                                                                         121
                                                                                                                                                                                          121
                                                                                                                                                                                                                                                          ABR55872;
                                                             Query Match
                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                               ABR5587
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to the truncated glycan, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSF) peptide, interferon alpha peptide, interferon beta peptide, erythropoieth cator interferon alpha peptide, follicle stimulating hormone peptide, erythropoieth (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF) peptide, interferon-gamma peptide, tissue plasminogen activator (GM-CSF) peptide, interferon-gamma peptide, tissue plasminogen activator (TPA) peptide, interleukin-2 (IL-2) peptide, factor VIII peptide, TNFalpha receptor/immunoglobulin (IS) G fusion peptide, urokinase peptide, anti-corporate in ID/IIIa moncolonal antibody peptide, chimeric anti HER2 antibody peptide, recombinant DNase peptide, chimeric anti-HER2 consulin peptide, hepatitis B surface antigen (HGBA), human growth hormone (HGH) peptide, and a modifying group, where the modifying group is covalently attached to the peptide through an intact glycosyl linking group. The method is useful for a cell-free, in vitro method of remodeling the above mentioned peptides. The present sequence represents the murine anti-CD20 antibody light chain mature variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGSSPREWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGSSPKPWIYGTSTLASGVPTRFSGSGGTSYSLTISRVEADDAATYYCQQWSSNPFTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B cell lymphoma; chimeric anti-CD20 antibody; cytostatic; mouse; VL; expression vector; murine; light chain; variable region.
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/label= Mature_anti-CD20_antibody_VL_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reff ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine anti-CD20 antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 572; DB 6;
Pred. No. 1.8e-34;
2; Mismatches 11.
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leonard JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU08393 standard; protein; 128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.8%;
Matches 114; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SGTKLEI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002197255-A1
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Rastetter WH;
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Peptide
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Claim 31; SEQ ID NO 12; 200pp; Japanese.

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                         Treating B cell lymphoma in humans, comprises administering immunologically active, chimeric anti-CD20 antibodies and/or radiolabeled anti-CD20 antibodies to the human.
                                                                                                                                                                                                                                                                                                                                                                                                                       PGSSPKPWIYGTSTLASGVPTRFSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                           The present invention relates to a method for treating B cell lymphoma. The method comprises administering at a first administration period, an immunologically active, mouse/human chimeric anti-CD20 antibody and/or administering, at a second administration period, a radiolabelled anti-CD20 antibody, to the human subject. The invention also discloses expression vectors that may be used in the method of the present invention. The method is useful for treating B cell lymphoma in humans. The present sequence represents murine anti-CD20 antibody light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody binding to CD20 and having Pc-bound sugar chains of low fucose content for treatment of cancer and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTWTCRASSSVSYIHWFQQK
                                                                                                                                                                                                                                                                                                                                              MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressant; cytostatic; antibody; CD20; N-acetylglucosamine; sugar chain; fucose; N-acetylglucosamine; sugar chain; cancer; immune disorder.
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                                                                                                                                                                                                                                                                                       Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Satoh M,
                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse anti-CD20 antibody light chain variable region.
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                                                                                                                                                                                                                                                                                     Score 572; DB 6;
Pred. No. 1.8e-34;
                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uchida K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC66268 standard; protein; 128 AA.
                                                                                   Example; Fig 4; 51pp; English
                                                                                                                                                                                                                                                                                  87.2%;
89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-DEC-2001; 2001JP-00392753.
09-APR-2002; 2002JP-00106948
01-NOV-2002; 2002JP-00319975.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                   Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
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                                                                                                                                                                                                                                                                                                    Best Local Similarity
 N-PSDB; ABX94206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GGTKLEI
                                                                                                                                                                                                                                                          Sequence 128 AA;
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                                                                                                                                                                                                                             variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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The invention relates to cells producing an antibody molecule specifically binding to CD20 are new, in which the antibody contains Neglecifically binding to CD20 are new, in which the antibody contains Neglecoside bond complex sugar chains bonded to the Region of the antibody peptide chains, of which less than 20% have a fucose residue bonded to the Neacetylgiucosamine residue at the reducing end of the sugar chain. The cells are used in the treatment and prevention of cancer and immune disorders. This sequence corresponds to a protein used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an improved method for treating B cell lymphoma comprising administering an anti-CD20 antibody. The improvement comprises administering at least one chemotherapeutic agent. The antibody causes a substantial depletion of peripheral B cells. The antibody is chimeric anti-CD20 or C2B8. The method is useful for treating B cell lymphoma.
                                                                                                                                                                                                                                                                                                                                           61 PGSSPKPWIYGTSTLASGVPTRFSGSGGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                           PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVBABDAATYYCQQWTSNPPTFG 120
                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                              MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGRKVTMTCRASSSVSYIHWFQQK 60
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                                                                                                                                                                                                                                                                            1 MDFQVQIPSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B cell lymphoma, anti-CD20, peripheral B cell; C2B8;
Immunoglobulin light chain variable region; mouse; antibody
                                                                                                                                                                                                                                         11, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine immunoglobulin light chain variable region.
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                                                                                                                                                                                                           Score 572; DB 7;
Pred. No. 1.8e-34;
                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; SEQ ID NO 7; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanna N, Leonard JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             least one chemotherapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE85686 standard; protein; 128
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93US-00149099.
97US-00921060.
                                                                                                                                                                                                           87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                            Best Local Simitation Watches 114; Conservative
                                                                                                                                               method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                            121 SGTKLEI 127
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                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTKLEI
                                                                                                                                                                            Sequence 128 AA;
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03-NOV-1993;
29-AUG-1997;
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Rastetter WH;
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ADE85686
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Length 128;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to cells with modified sugar chain modifying enzyme activity. The enzyme activity of binding the l-position of fucose to the 6-position of an N-acetylglucosamine at the reducing end of a complex N-glycoside linked sugar chain via an alpha-bond is absent or less than in the parent cell. The sugar chain modifying enzyme is preferably alpha 1,6-fucosyltransferase (ADE73052-ADE73053 and ADE73055-ADE73066). The invention is useful for the treatment and prevention of tumours, allergy, inflammation, autoimmune disease, circulatory disparance was used in an example from the invention. The present sequence was
                                                                                                                                                                                                                                     120
                                                                                                                                                                                                        PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                          9
                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cells with reduced or absent alpha 1,6-fucosyltransferase activity for treatment of tumors, allergy, inflammation, autoimmune disease, circulatory disorders, and viral and bacterial infection.
                                                                                                                                                                                                                        1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQK
                                                                                                                                        1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
This sequence represents a murine immunoglobulin light chain variable region used in the method of the invention.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antiallergic; Anti-inflammatory; Immunosuppressive; Antibacterial; Antiviral; Cytostatic; enzyme; alpha 1,6-fucosyltransferase; tumour; allergy; inflammation; autoimmune disease; circulatory disorder; viral infection; bacterial infection; murine.
                                                                                                             ;
0
                                                                            Length 128;
                                                                                                             11; Indels
                                                                              Score 572; DB 7;
Pred. No. 1.8e-34;
                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 164-165; 187pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mori K, Yamano K;
                                                                                                                                                                                                                                                                                                                                                                               ADE73083 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-2003; 2003WO-JP004507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine FUT8-related sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002; 2002JP-00106953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                              87.2%;
89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                           Matches 114; Conservative
                                                                                                                                                                                                                                                                                                 127
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                                                                                                                                                                                                                                                                    SGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Satoh M,
                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                       GGTKLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADE73068.
                                                Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003085107-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamane N,
                                                                                                                                                                                                                                                                                                                                                                                                              ADE73083;
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                                                                               Query Match
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Sequence 128 AA;

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The invention relates to a drug containing as the active ingredient, an antibody composition produced by cells tolerant to a lectin recognising a sugar-chain structure in which an alpha-bond is formed between the 6-position of N-acetylglucosamine at the reducing end of an N-glycoside bond-type complex sugar chain and the 1-position of fucose. The drugs are useful in screening and treating patients not suitable for drugs not preventives or remedies for diseases accompanying tumour, allersy or inflammation, autonmence diseases, diseases of the circulatory system, and viral or bacterial infections. In a method from the invention, a CCR4 gene was used for constructing a vector (CAG-CCR4/pcDNAs) for producing a transformant EL-4 cell (ATC TEB-39) to express chimeric CCR4. Antibody-dependent cytotoxicity of the thus produced antibody composition was confirmed. The current sequence represents a protein related to the
                                    ö
                                                                                                                                                            61 PGSSPKPWIYATSNIASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
                                                                                                                                         PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVBABDAATYYCQQWSSNPFTFG 120
                                                                      9
                                                                                        brugs containing antibody compositions produced by cells tolerant to lectin recognizing specific sugar-chain structure, useful in screening and treating patients not suitable for drugs not derived from these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; antiallergic; immunomodulator; cardiant; virucide; antibacterial; drug; antibody; lectin; N-acetylglucosamine; fucose; tumour; allergy; inflammation; autoimmune disease; circulatory system; viral; bacterial; infection; CCR4.
                                                                    1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK
                                      Gaps
                                    ö
                                    Indels
                                      11;
Score 572; DB 7;
Pred. No. 1.8e-34;
2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; SEQ ID NO 6; 157pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein related to the invention #1
                                                                                                                                                                                                                                                                                                                                      ADF60660 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-2003; 2003WO-JP004503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2002; 2002JP-00106949.
Query Match 87.2%;
Best Local Similarity 89.8%;
Matches 114; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2004 (first entry)
                                                                                                                                                                                                              121 SGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-812676/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Niwa R, Shitara K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADF60645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003084569-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                     ADF60660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                remodelling and glycoconjugation of these naturally occurring peptides thereof. Specifically, each BPO peptide comprises one or more glycans and has a glycoconjugate molecule such as polyethylene glycol (PEG) attached to it. Accordingly, the present invention provides glycobEGylated BPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptides that have either monoantennary, biantennary or triantennary peptides that have either monoantennary, biantennary or triantennary glycans covalently attached thereto. As such, these peptides are useful for the treatment of anaemia, and hence exhibit antianaemic activities working to increase haematocrit levels in mammals, in particular in humans i.e. increasing the relative volume of blood occupied by erythrocytes. Furthermore, EPO therapy can be used to treat kidney dialysis patients. This polypeptide is a human protein sequence related to the field of haematology, given in an exemplification of the invention.
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                                                                                                MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQK
                                                                 MDPQVQIPSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to novel erythropoietin (EPO) peptides and the
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Mature variable light chain anti-CD20 murine antibody protein SeqID
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse; murine; antibody; erythropoietin; BPO; glycoconjugation;
glycoPEGylated BPO peptide; anaemia; antianaemic; haematocrit level;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel erythropoietin peptide comprising one or more glycans, having glycoconjugate molecule covalently attached to peptide, useful for treating anemia in mammal such as human.
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   Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen X;
                                  11; Indels
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 Score 572; DB 7;
Pred. No. 1.8e-34;
2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 60; 1018pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    υÌ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoPEGylated BPO peptide; anaemia
kidney dialysis; haematology; CD20.
                                                                                                                                                                                                                                                                                                               ADN49732 standard; protein; 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2002; 2002US-00287994.
06-JAN-2003; 2003US-00360770.
19-FEB-2003; 2003US-00360779.
 89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003US-00410945
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frees S, Zopf D,
                                                                                                                                                                                                SGTKLEI 127
                                                                                                                                                                                                                              121 GGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004-399848/37.
                 Similarity
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N-PSDB; ADN49731
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09-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39-OCT-2002;
                                Matches 114;
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Query Match
Best Local
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ADN49732
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61 PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
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                                                                                                                                                  61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                              Hemostatic; Hepatotropic; Antianemic; Cytostatic; Osteopathic;
Antibacterial; Respiratory-Gen.; Antiinflammatory; Nephrotropic;
Antiinfertility; Antitubercular; Tuberculostatic; protein engineering;
bleeding; factor VIII deficiency; factor IX deficiency; liver cirrhosis;
infertility; anemia; end-stage renal disease; acute myelogenous leukemia;
osteoporosis; pulmonary fibrosis; tuberculosis.
                                                                                          1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK 60
                                                                                                            1 MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTWTCRASSSVSYIHWFQQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell-free in vitro method of remodeling peptide comprising poly(ethylene glycol) useful for generating glycopeptide suitable for therapeutic uses in mammal, involves addition or deletion of glycosyl groups to peptide.
                                                                  Gaps
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                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X;
                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hakes D,
                                    Score 572; DB 8;
Pred. No. 1.8e-34;
2; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                    Mouse anti-CD20 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 60; 1024pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowe C,
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                                                                                                                                                                                                                                                                                                     ADU74408 standard; protein; 128
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2003US-00410930.
2003US-00410945.
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2003US-00410980.
2003US-00410997.
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                                     87.2%;
89.8%;
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                                                                Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zopf D,
                                                                                                                                                                                                      121 SGTKLEI 127
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                                                     Similarity
                                                                                                                                                                                                                                  121 GGTKLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADU74407.
            Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004099231-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-2003;
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                                      Query Match
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ADU74408
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peptide comprising poly(ethylene glycol). (MI) is useful for remodeling protein to generate glycopeptide having desired glycosylation pattern suitable for therapeutic use in mammal. (MI) is useful for remodeling peptides chosen from immunoglobulin, erythroposetin, tisue-type activator peptide, etc. (MI) is useful for remodeling (a) G-GSF which is useful for treating acute myeloid leukemia (AML), non-myeloid cancer patient receiving bone marrow transplant, (b) factor VII for treating bleeding episode, factor VIII deficiency, factor IX deficiency, liver cirrhosis, (c) FSH for patients undergoing intrauterine insemination, in vitro fertilization and for infertile patient, (d) EPO for treating anemic patient baving chronic renal insufficiency and end stage remains acute myelogenous leukemia, (f) IFN-gamma for treating malignant osteoporosis, pulmonary fibrosis, tuberculosis, cryptococcal meningitis, etc. The glycopeptide produced using (MI) has specific customized or desired glycosylation pattern. (MI) allows efficient production of improved therapeutic moiety. The present sequence represents the amino acid sequence of a protein remodelled in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PGSSPKPWIYATSNLASGVPVRFSGSGGTSYSLTISRVEABDAATYYCQQWTSNPPTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDFQVQIISFLLISASVIMSRGQIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTWTCRASSSVIYMCWNQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      Score 572; DB 8; Length 128;
Pred. No. 1.8e-34;
2; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        87.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGTKLEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                         Sequence 128 AA;
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Novel cell that is neutralized to serum-free medium and carrying knockout of gene encoding enzyme involved in carbohydrate modification, useful for

Kusunoki M, Kinoshita S;

Urakubo M,

Satoh M, Iida S,

Nakano R, Ohnuki N;

WPI; 2005-346214/35.

(KYOW ) KYOWA HAKKO KOGYO KK. 09-OCT-2003; 2003JP-00350166

38-OCT-2004; 2004WO-JP015315.

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nedium and carrying a knockout genome gene encoding an enzyme which participates in a sugar chain modification, where fucose is linked by an alpha linkage at the l-position to the 6-position of N-acetylglucosamine to the reducing end of an N-glycoside-binding complex sugar chain. Also described are: a neutralization (MI) method of cell to the serum free medium; cloning, after making neutralizing cell to the serum free medium by (MI); a cell having a knocked out genome gene encoding the enzyme which is involved in the carbohydrate modification that is neutralized to the serum free medium; and a cloned cell strain, composition having a knocked out genome gene encoding the enzyme which is involved in the carbohydrate modification that is neutralized to the serum free medium.

(I) is useful for manufacturing a glycoprotein composition, which is unclease and in a culture medium and collecting the accumulated glycoprotein composition from the culture medium. The glycoprotein composition is useful in drug discovery and for treating immunological
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                                                                                                                                                                                                                                                                                                                                                                                                                 disease such as cancer, inflammatory disease, autoimmune disease, allergy, circulatory disorder, virus or bacterial infection. This is the amino acid sequence of a polypeptide used in the creation of host cells capable of producing glycoprotein compositions useful in drug discovery.
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manufacturing glycoprotein composition useful in treating, e.g. cancer
                                                                                   to a serum-free
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 128;
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                                                                                 invention describes a cell (I) that is neutralized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.2%; Score 572; DB 9;
89.8%; Pred. No. 1.8e-34;
iive 2; Mismatches 11;
                                          Disclosure, Page 122-123; 135pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C2B8 antibody light chain protein.
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16-NOV-2001; 2001US-0331481P.
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 128 AA;
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                                                                                                                                                     Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2BB antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2BB construct where the CH2 domain has been deleted. Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-Hodgkin's lymphoma. Antibodies of the invention are also used to treat neoplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tumour size, inhibiting tumour growth and/or useful for reducing the aurivial time of funour-bearing animals and for treating tumours. The present sequence is human C2BB light chain protein. This sequence is used in the exemplification of the invention
                                             Novel domain deleted CC49 antibody reactive with tumor associated antigen -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.
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thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
                                                                                                                                         present invention relates to domain deleted CC49 or C2B8 antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%; Score 572; DB 5; Length 235; 89.8%; Pred. No. 3.2e-34; ive 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dermatological; immunosuppressive; antiinflammatory
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                                                                                                          Example 1; Fig 3B; 74pp; English
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16-NOV-2001; 2001US-0331481P.
21-DEC-2001; 2001US-0341858P.
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WPI; 2002-698547/75.
N-PSDB; AAD45754.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 235 AA;
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ABB82834
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(IDEC-) IDEC PHARM CORP

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The invention relates to a dimeric antibody (1) comprising several monomeric subunits, where the monomeric subunits are non-covalently associated. (I) is useful for treating a disorder, especially immune disorder, and neoplastic disorder such as relapsed Hodgkin's disease, resistant Hodgkin's disease high grade, low grade and intermediate grade non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL), lymphoplasmacyroid lymphoma (LPL), mantle cell lymphoma (MCL), Gollicular lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma, AIDS-related lymphoma, monocytic B cell lymphoma, angioimmunoblastic lymphodenopathy, small lymphocytic, follicular, diffuse large cell, diffuse small cleaved cell, large cell immunoblastic lympholastic lympholastic lymphomas, and non-Burkitt's, follicular, mixed small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
                                                                                                                                                   neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PGSSPKPWIYATSNLASGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a detailed description of the various uses of (1)). The present sequence represents the antibody C2B8 light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDFQVQIPSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK
                                                                                                                                                                               disorder, has several non-covalently associated monomeric subunits
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                                                                                                                                               Novel dimeric antibody useful for treating immune disorder and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.2%; Score 572; DB 6; Length 235; 89.8%; Pred. No. 3.2e-34; ive 2; Mismatches 11; Indels
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fungicide; viral infection; virucide; parasitic infection;
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Hariharan K;
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Chinn P,
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Best Local Similarity 89.8
Matches 114; Conservative
Braslawsky GR, Hanna N,
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                                                         2003-140446/13.
                                                                                         N-PSDB; ABZ24018
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Sequence 500 AA;

X S

24-FEB-2005.

24-DEC-2003; 2003WO-US041600.

26-JUL-2003; 2003US-00627556

(TRUB-) TRUBION PHARM INC

Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

WPI; 2005-182370/19. N-PSDB; ADY21924.

New non-naturally occurring single chain protein comprising polypeptides with bindaing domain, connecting regions and N-terminally truncated immunoglobulin, having immunological activity, useful for neutralizing infectious agent.

Disclosure; Page 383; 590pp; English

The invention relates to a non-naturally occurring single chain process.

(1) comprising a first polypeptide having a binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide capable of binding to a target molecule, the binding domain polypeptide capable of binding a connecting region, which comprises an amino acid substitution or deletion at one or more amino acid residues, as second polypeptide comprising a connecting region attached to the first protein is capable of an immunological activity. Also included are reducing a target cell population in a subject (involving administering to the subject a protein that is less than 150 kb, which involves treating the target cell population with a first protein or peptide that capable of at least one of binding an Foresing protein or peptide that capable of at least one of binding an Foresing protein or peptide molecule is directly connected to the second protein or peptide molecule is directly connected to the second protein or peptide molecule and the expectation or peptide molecule is directly connected to the second protein or peptide molecule are linked by a third protein or peptide molecule and the molecule are linked by a third protein or peptide molecule of the molecule are linked by a third protein or peptide molecule of the molecule are linked by a third protein or peptide molecule are linked by a protein or peptide molecule or reperior connected trunk, a cell containing the polypeptide, are combinant when the composition a cell containing the polypeptide, are recombinant well or manimal), a polymuclecide that encodes the polypeptide of the an animal, a cell containing the polypeptide, are recombinant well or expressing the polypeptide, are recombinant with a cell containing the polypeptide, are recombinant with one capable of expressing the polypeptide, are composition, a cell containing the polypeptide in comprisation comprising protein having (TN/CT) of caspase-3, caspase-8 or CD80. The fusion polypeptides are useful for neutralization of an infectious agent (where the infectious agent is a bacterium, a virus, a parasite, or a fungus) and also for treatment of cancer, immune disorders, Grave's disease, Hashimoto's disease, rheumatoid arthritis, systemic lupus erythematosus, Sjoegren's syndrome, thrombocytopenic purpura, multiple sclerosis and myasthenia gravis. The present sequence represents a fusion protein of the the invention relates to a non-naturally occurring single chain protein

invention

61 PGSSPKPWIYGTSTLASGVPTRFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPFTFG 120 61 PGSSPKPWIYAPSNIASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFG 120 9 1 MDFQVQIFSFLLISASVILARGQIVLSQSPAILSASPGEKVTWTCRASSSVSYMHWYQQK 1 MDFQVQIFSFLLISASVIMSRGQIVLSQSPAILFASPGETVTMTCRASSSVIYMCWNQQK Gaps ö Length 500; 11; Indels Score 567; DB 9; Pred. No. 1.6e-33; 4; Mismatches 11; 86.4%; Best Local Similarity 88.2 Matches 112, Conservative SGTKLEI 127 121 Query Match ઠ ઠે 유 ð

Search completed: March 20, 2006, 07:35:40 Job time : 48.9655 secs

121 AGTKLEL 127